Seguence

Sequence 49, Appl Sequence 9193, Ap Sequence 9193, Ap Sequence 10543, A Sequence 11154, A Sequence 11572, A Sequence 11873, A Sequence 12042, A Sequence 12047, A Patent No. 5187777 Sequence 61551, A Sequence 61

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US-08-468-576B-18
) Sequence 18, Application US/08468576B
) Patent No. 5953145
) GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
) TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
CORRESPONDENCES: 19
CORRESPONDENCE ADDRESS:
) CORRESPONDENCE ADDRESS:
) STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette; 3.50 inch, 1.4 Mb storage computer Apple Macintosh coperating System 7.5 SOFTWARE: Wordberfect CURRENT Apple Mordberfect CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/468,576B FILING DATE: OG-JUN-1995 CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/468,576B FILING DATE: OS-JUN-1995 CLASSIFICATION DATA:

APPLICATION NUMBER: US/08/39,276 FILING DATE: OS-JUN-1992 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/372,646 FILING DATE: OS-JUN-1992 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/441,703 FILING DATE: 04-DEC-1989 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/441,703 FILING DATE: 04-DEC-1989 PRIOR APPLICATION NUMBER: US/07/312,543 FILING DATE: 17-PEB-1989 ATTORNEY/AGENT INFORMATION:

NAMMER: WITHER READERSTANDER: US/07/312,543 FILING DATE: 17-PEB-1989 ATTORNEY/AGENT INFORMATION:

NAMMER: WITHER READERSTANDER: US/07/312,543 FILING DATE: 17-PEB-1989 ATTORNEY/AGENT INFORMATION:

NAMMER: WITHER OF DEC-1989
US-09-876-527-16
US-09-552-8028-49
US-09-489-039A-9959
US-09-489-039A-10543
US-09-489-039A-11154
US-09-489-039A-11154
US-09-489-039A-11572
US-09-489-039A-11572
US-09-489-039A-11572
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US-09-489-039A-11572
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US-09-489-039A-12042
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                                                                                                                                                                      US-09-270-767-43882
US-09-270-76-61551
US-09-252-991A-24690
PCT-US95-08493-15
PCT-US95-08493-2
                                                                                                                                                                                                                                                                   ALIGNMENTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KURT G. BIISCOE
REGISTRATION NUBBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 25
TELECOMMUNICATION INFORMATION:
TELEFAX: (914) 332-1700
TELEFAX: (914) 332-1700
TELEFAX: (914) 032-1844
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 amino acids
                             CITY: Tarrytown
STATE: New York
COUNTRY: USA
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                                                                                        October 28, 2004, 11:13:25 ; Search time 22.2651 Seconds (without alignments) 83.400 Million cell updates/sec
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(GGT2 6/ptodata1/iaa/6B_COMB.pep:*

(GGT2 6/ptodata1/iaa/BCOMB.pep:*

(GGT2 6/ptodata1/iaa/PCTUS COMB.pep:*

(GGT2 6/ptodata1/iaa/PCTUS COMB.pep:*
                GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
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US-08-468-579B-19

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US-09-552-802B-21

US-09-552-802B-19

US-08-811-481-7

US-08-811-481-2

US-08-848-159-5

US-08-811-481-2

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-08-884-569A-2
-08-811-481-16
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28
1 LAKEWQALCAYQAEPNTCATAQGEGNIK 28
                                                                                                                                                                                                                                        478139 seqs, 66318000 residues
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                                                                   OM protein - protein search, using sw model
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length: 2000000000
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Maximum DB
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67 LAKEWQALCAYQAEPNTCATAQGEGNIK 94
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                                                              RESULT 3
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                                                                                      100.0%; Score 28; DB 2; Length 294; ilarity 100.0%; Pred. No. 6.3e-22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                            Sequence 18, Application US/08468579B
Factor to 2981700
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 10591-5144
ZIP: 10591-5144
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kurt G. Briscoe
REGISTRATION WUNBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                            1 LAKEWQALCAYQAEPNTCATAQGEGNIK 28
                                                                                                                                                                                                                      67 LAKEWQALCAYQAEPNTCATAQGEGNIK 94
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APPLICATION DATA
APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-WAY-1994
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-UN-1992
RICH APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-UN-1991
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
FILING DATE: 07-DEC-1989
FILING DATE: 17-FEB-1989
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,579B
FILING DATE: O6-JUN-1995
CLASSIFICATION: 530
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TELEPAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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LACTERISTICS:
294 amino acids
17PE: amino acids
10POLOGY: linear
US-08-468-579B-18
Querv
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STREET: 660 ...
CITY: Tarrytown
TYPE: amino acid
TOPOLOGY: linear
                                                                                      Query Match
Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                                                                                                                                     RESULT 2
US-08-468-579B-18
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US-08-468-576B-18
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Sequence 18, Application US/08468577B
Patent No. 601804
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSES: Sprung Kramer Schaefer & Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-468-576B-19
Sequence 19, Application US/08468576B
Patent No. 5955345
GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
SOFTWARE: Wordberfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,577B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 28; DB 3; L
Best Local Similarity 100.0%; Pred. No. 6.3e-22;
Matches 28; Conservative 0; Mismatches 0;
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660 White Plains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67 LAKEWQALCAYQAEPNTCATAQGEGNIK 94
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PILING DATE: 06-JUN-1995
CLASSIPICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,276
PILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: O8-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
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FILING DATE: 14-UNN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/41,703
FILING DATE: 04-DEC-1989
FRIOR APPLICATION DATA:
APPLICATION DATA: US 07/312,543
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Kurt G. Briscoe
REGISTRATION NUMBER: 33,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (914) 332-1844 INFORMATION FOR SEQ ID NO: 18:
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amino acid
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                                                                                                                                                                                                                                                 STREET: 660 White
CITY: Tarrytown
STATE: New York
COUNTRY: USA
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10591-5144
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1 LAKEWQALCAYQAEPNTCATAQGEGNIK 28

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Sequence 10, Application US/08105904B
; Patent No. 6001364
GENERAL INFORMATION:
    GENERAL INFORMATION:
    APPLICANT: Rose, Keith
    APPLICANT: Robin
    TITLE OF INVENTION: HETERO-POLYOXIME COMPOUNDS AND THEIR
    TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
    NUMBER OF SEQUENCES: 24
    CORRESPONDENCE ADDRESS:
    ADDRESSEBE: Cooley Godward Castro Huddleson & Tatum
    STREET: 5 Palo Alto
    CITY: Palo Alto
    STATE: California
    COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZUDITER: U.S.A.
ZUDITER: U.S.A.
ZUP: 94306
COMPUTER: READABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/105,904B
FILING DATE: 31-AUG-193
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/057,594
FILING DATE: 05-MAY-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: ABIC-001/02US
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION INFORMATION:
TELECOMMONICATION OF SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acids
TTYPE: amino acids
TOWNED 
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US-08-105-904B-10
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Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 17, Appl
Sequence 2, Appli
Patent No. 5514646
Sequence 24, Appl
Sequence 3, Appli
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Sequence 4, Ag
Sequence 3, Ag
Patent No. 5457
Sequence 13, A
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Sequence 3,
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(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
? /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
? /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
? /cgn2_6/ptodata/1/iaa/ReCOMB.pep:*
?: /cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
?: /cgn2_6/ptodata/1/iaa/PcTuS_COMB.pep:*
                               GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
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US-08-53-928-10
US-09-633-928-10
US-09-634-64-17
US-09-639-641-2
US-09-639-67-787-2
US-09-639-67-2
US-08-160-3
US-08-160-3
US-08-18-3
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US-09-947-563-3
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US-08-114-877A-10
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US-07-715-183C-1
US-09-477-924-2
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-09-676-787-7
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US-09-134-836-5
US-09-386-303A-4
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 200000000
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11
1 QPLALEGSLQK 11
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Perfect score:
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Sequence 11,
Sequence 2,
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Seguence 2,
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Sequence 2,
      US-09-947-563-4
US-09-947-563-5
US-08-389-487-7
US-09-099-307-7
US-09-099-307-1
US-09-099-307-1
US-09-099-307-1
US-09-099-307-1
US-09-099-307-1
US-09-701-968-8
US-09-701-968-9
US-09-701-968-9
US-08-589-028-2
US-08-589-028-2
US-08-589-028-4
US-08-784-582-4
US-08-784-582-4
US-08-784-582-4
US-08-785-21-2
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Fatent No. 6174530
GENERAL INFORMATION:
APPLICANT: Rose, Keith
APPLICANT: Rose, Keith
TITLE OF INVENTION: HOMOGENOUS POLYOXIME COMPOSITIONS AND THEIR
TITLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEBE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
COUNTRY: California
COUNTRY: U.S.A.
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  ch 100.0%; Score 11; DB 3; Length 23 Similarity 100.0%; Pred. No. 3.9e-05; 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,877A
FILING DATE: 31-AUG-1993
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/057,594
FILING DATE: 05 MAX-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE/DOCKET NUMBER: ABIC-001/01US
TELEPHONE: (415) 843 5070
TELEPHONE: (415) 857-0663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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COTHER INFORMATION: AOA-Glu
US-08-114-877A-10
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amino acid
GY: linear
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Query Match
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RESULT 3 US-08-537-928-10 F Sequence 10, Application US/08537928

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PRESENTED NO. 4217873

RESIDENT NO. 4217873

RESIDENT NO. 4217873

REPRINTED NO. 4217873

CURRENT FILING DATE: 1996-01-05

EMALIER FILING DATE: 1997-05-01

EMALIER FILING DATE: 1997-05-01

EMALIER FILING DATE: 1997-05-01

EMALIER FILING DATE: 1997-06-01

EMALIER FILING DATE: 1997-00/1318

CONTRAINT MARIENGEN DATE: EMALIER FILING DATE: 1997-06-31

FILING DATE: EMALIER FILING DATE: 1997-06-31

FEAURTH OF THE PRESENCE: CREATER FILING DATE: 1997-06-31

FEAURTH OF THE PRESEN
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Adf17074 Human alb Aap40829 Sequence Aar20709 Modified Aar22327 Modified Aar22331 Modified Aar22331 Modified Aar22332 Proinsuli Aar20694 Modified Aar22256 Modified Aar22256 Modified Aar2225 Modified Aar22236 Modified Aar22239 Modified Aar20705 Proinsuli Aar20709 Modified Aar20709 Modified Aar20709 Modified Aar20709 Modified Aar20709 Modified Aar20709 Modified Aar20709 Proinsuli

score:

Perfect

OM protein

Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

Database :

Result

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Bridging peptides (AAW06808 and AAW00872) are utilised in novel single chain peptides of formula b-BP-a (see also AAW06806-07), where b is the insulin B-chain or its analogue, BP is a bridging peptide, and a is the insulin A-chain or its analogue. These peptides show high insulin bioactivity. Suitable bridging peptides should not contain sequences that interact with the IGF-I receptor, nor should they contain cleavage sites. They are preferably derived from the C-peptide of human proinsulin so as to minimise potential immunogenicity, and most preferably consist of amino acids 54-65 of the C-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         used for treating diabetes.
                                                                                                                                                                                                                                                                                                        Single chain insulin; diabetes mellitus; gene therapy
                                                                                                                                                                                                                                                                                       Single chain insulin polypeptide bridging peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 53; DB 2; L
100.0%; Pred. No. 0.00059;
ive 0; Mismatches 0;
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               AAR20710
AAR20699
AAR22327
AAR22330
                                                 AAR22331
AAR22332
AAR20694
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AAR20707
AAR22326
AAR22336
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AAR20704
AAR20692
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AAR20693
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                                                                                                                                                                                                                                     AAW06808 standard; peptide; 12
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95US-00435762
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Matches 11; Conservative
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(ELIL ) LILLY & CO ELI
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Sequence 12 AA;
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05-MAY-1995;
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AAW06808;
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070766666666666444444
07076666666666444444
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Aau02065 Synthetic
Aap70639 Sequence
Ada01446 Amino aci
Aap60248 Human pro
Aar20711 Ser Al3,
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Aaw81858 Human pro
Adn34533 Preproins
Aap50011 Sequence
Aar83840 Part of i
Aap40830 Sequence
Aar68897 Human ins
Aay98003 Human ins
Aay98003 Human ins
Aay665687 Fragment
Aag65687 Fragment
Aag65687 Fragment
Aag65687 Fragment
Aar38432 Split (64)
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Adi29027 Proinsuli
                                                         ; Search time 38.8313 Seconds (without alignments) 101.620 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                           2002273
          GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                        2002273 segs, 358729299 residues
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Maximum Match 100%
Listing first 45 summaries
                                           - protein search, using sw model
                                                             2004, 06:03:19
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AAP70639
ADQ91446
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AAW81858
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L: geneseqp1980s:*
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53
1 QPLALEGSLQK 11
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Length 12; Indels

Miller AR

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The present invention describes an isolated MHC class II compound (I) comprising: (a) an MHC class II component comprising at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II alpha chain and at least a portion of an MHC class II beta chain, such that the MHC class II alpha chain and MHC class II beta chain form a peptide binding groove; (b) a spaceholder molecule; and (c) an effector component. Also described: (l) a pharmaceutical composition comprising the MHC class II molecule and a carrier; (2) a method of producing an MHC class II molecule and a carrier; (2) a method of an antigen-specific T cell; (4) a method of regulating an immune response in a subject; (s) a method of treating an immune disorder in a subject; (d) a method of treating an immune disorder wive in a subject; (i) a method of treating an immune disorder wive in a subject; (i) a method of treating an immune disorder wive in a subject; (I) has virucide, antibacterial, antiparasitic, cytostatic and immune classive citivities, and can be used in gene therapy. The MHC class II compound (I) can be used for preparing a composition for treating immune disorders, neoplastic disease, autoimmunity or toxicity. The present sequence represents a peptide which can be used to generate peptide wince is precific.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MHC class II compound; MHC class II component; MHC class II alpha chain; MHC class II beta chain; peptide binding groove; spaceholder molecule; effector component; immune response; immune disorder; virucide; antibacterial; antiparastic; cytostatic; immunosuppressive; gene therapy; viral infections; bacterial infection; parastic infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New MHC class II compound, useful for preparing a composition for treating immune disorders e.g. viral infections, bacterial infections, parasitic infections, neoplastic disease, autoimmunity or toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy, viral infections, bacterial ineoplastic disease, autoimmunity, toxicity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proinsulin (73-90) peptide SEQ ID NO:23.
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                                                                                                                                                                                                                                                                     ADI29027 standard; peptide; 18 AA.
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22-JUL-2002; 2002US-0397893P
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Synthetic.
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Score 53; DB 8; Length 18; Pred. No. 0.00094;

100.0%;

Query Match . Best Local Similarity

Sequence 18 AA;

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Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - used for
                                                                                                                                                                                                                Polyoxime, homopolyoxine, heteropolyoxime, peptide presentation, cell imaging, complementary orthogonal specifically active molecule, COSM, baseplate, proinsulin-C; insulin, immunogen.
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Indels
                                                                                                                                                                                                                                                                                                                             /note= "aminooxyacetyl-glutamic acid"
ö
Mismatches
                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 53; 85pp; English.
                                                                                                        AAR60842 standard; peptide; 23 AA.
                                                                                                                                                                                          AcA-PepC COSM polyoxime component.
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93US-00105904.
93US-00114877.
                                                                                                                                                                                                                                                                                                               /label= OTHER
                                                                                                                                                                                                                                                                                                                                                                                                    94WO-IB000093
                                                                                                                                                        (revised)
(first entry)
11; Conservative
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nes 11; Conservative
                     1 OPLALEGSLOK 11
                                            6 OPLALEGSLOK 16
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(OFFO/) OFFORD R E.
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                                                                                                                                                                                                                                                                                         Key
Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                  05-MAY-1994;
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31-AUG-1993;
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05-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1994.
                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                               AAR60842;
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October 28, 2004, 11:39:31; Search time 21.7349 Seconds (without alignments) 164.085 Million cell updates/sec
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(cgn2_6/ptodata/2/pubpaa/DCT_RW PUBCOMB.pep:*

(cgn2_6/ptodata/2/pubpaa/PCT_RW PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/DCT_RW PUB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO6_PUBGOMB.pep:*

(cgn2_6/ptodata/2/pubpaa/USO8_RW PUB.pep:*

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1370721 segs, 324215800 residues
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                                                                                                                       OM protein - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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11
1 QPLALEGSLQK 11
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Perfect score:
Sequence:
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                                                                                                                                                                                        Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Sequence 23, Appl	Sequence 24, Appl	Sequence 4, Appli	Sequence 3, Appli	Seguence 4, Appli	Sequence 13, Appl	Sequence 13, Appl	Sequence 1, Appli	Sequence 4, Appli	Sequence 2, Appli	4,	Sequence 2, Appli	Sequence 4, Appli
	ID	US-10-617-568-23	US-10-641-834-24	US-09-815-229-4	US-09-947-563-3	US-10-740-098-4	US-09-815-229-13	US-10-740-098-13	US-09-878-380-1	US-09-858-935B-4	US-10-028-410-2	US-10-054-873-4	US-10-444-326-2	US-10-271-869-4
	DB	17	17	თ	σ	16	σ	16	σ	10	13	13	14	14
	Query Match Length DB	18	33	35	35	ខេ	54	54	98	98	98	86	86	98
æ	Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	11	11	11	11	11	11	11	11	11	11	11	11	11
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Sequence 2, Appli Sequence 2, Appli	Sequence 2, Appii Sequence 4, Appli		Sequence 125, App	Sequence 3, Appli	Sequence 9, Appli	Sequence 6, Appli	equence 12	٠,	(D	'n	o o	equence 2,	e 44	Sequence 44, Appl	eguence 44	4	equence 2(4	Sequence 44, Appl	4	4	m	e 47	63	equence 62,	,	quence 2,	equence 1	e)
-444-262 -444-649	5 US-10-444 US-09-947	US-09-947-5	0S-09	US-09-8	9-804-40	US-09-969-7	96-60	US-10-038-68	US-10-328-8	10-383-28	US-10-346-5	US-10-321-71	US-10-411-0	S US-10-411-026-44	US-10-410-9	US-10-411	US-10-700-7	US-10-410-9	US-10-41	6 US-10-411-012-44	US-10-28	US-10-740-09	10-410-	US-09-280-030	US-09-280-030-	US-09-269-43	US-09-878-38	5 US-10-430-752A-	US-10-430-7
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ALIGNMENTS

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Gaps
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0
Query Match
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                         6 QPLALEGSLOK 16
                                                                                                                                                                               1 OPLALEGSLOK 11
                                                                                                                      LENGTH: 18
TYPE: PRT
CRGANISM: Homo sapiens
US-10-617-568-23
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RESULT 2 US-10-641-834-24 ; Sequence 24, Application US/10641834

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APPLICANT: Filvarion:
APPLICANT: Filvarion:
APPLICANT: Chumu, Franklin W.
APPLICANT: Okumu, Franklin W.
TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS CURRENT FILMS PAPPLICATION NUMBER: US/10/740,098
CURRENT FILMS DATE: 2003-12-17
PRIOR APPLICATION NUMBER: US/09/815,229
PRIOR FILMS DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/192,103
PRIOR FILMS DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US 09947,563
FILING DATE: 07-569-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/134,836
FILING DATE: cUnknown>
ATTORNEY/AGENT INFORMATION:
NAME: Leslie McDonell
REGISTRATION NUMBER: 34,872
FELENGENCE/DOCKET NUMBER: 02481.1600-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: 1..35
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Escherichia coli
                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-10-740-098-4
; Sequence 4, Application US/10740098; Publication No. US20040138101A1
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 35 amino acids TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 OPLALEGSLOK 11
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                                                             STREET: 1300
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Matches 11; Conserv
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Best Local Similarity
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ORGANISM:
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APPLICANT: Rubroder, Reinhold
TITLE OF INVENTION: Improved process for obtaining
insulin precursors having correctly bonded cystine bridges
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Filvaroff, Ellen H.
APPLICANT: Filvaroff, Ellen H.
APPLICANT: Okumu, Franklin W.
TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS CURRENT APPLICATION NUMBER: US/09/815,229
CURRENT APPLICATION NUMBER: US 60/192,103
PRIOR APPLICATION NUMBER: US 60/192,103
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 17
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FUBLICATION NO. US20040209330A1
GENERAL INFORMATION:
GENERAL INFORMATION:
THOSELI, Stephen James
APPLICANT: Russell, Stephen James
APPLICANT: Russell, Stephen James
TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
CURRENT APPLICATION NUMBER: US/10/641,834
CURRENT FILING DATE: 2003-05-16
PRIOR APPLICATION NUMBER: 05/639,667
PRIOR APPLICATION NUMBER: 60/149,168
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 31
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 24
MANCHEN AND 34
MAN
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 33;
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100.0%; Score 11; DB 17;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 100.0%; Pred. No. 0.00067;
Matches 11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: C-peptide sequence US-10-641-834-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 4, Application US/09815229
Patent No. US20020058614A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/09947563; Patent No. US20020156234A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 OPLALEGSLOK 11
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-815-229-4
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101821 Sequence 6
AR07833 Sequence
A48809 Sequence
A48809 Sequence
27
AR069914 Sequence 27
AR069914 Sequence
E43909 Novel vecto
102917 Sequence 6
E00074 DNA sequence
114150 Sequence 14
114159 Sequence 12
114150 Sequence 14
114151 Sequence 14
114151 Sequence 14
114151 Sequence 14
114151 Sequence 16
A0082 Artificial
E43908 Novel vecto
M12913 Synthetic D
A11939 Nucleotide
112514 Sequence 42
11372 Sequence 43
11372 Sequence 44
11376 Sequence 44
107905 Sequence 47
107805 Sequence 47
107806 Sequence 47
107807 Sequence 47
107907 Sequence 47
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Unclassified.
Unclassified.

I (bases 1 to 68)
Shin,H.-C., Chang,S.-G., Kim,D.-Y. and Kim,C.-S.
Proinsulin derivative and process for producing human insulin
Patent: US 5962267-A 18 05-OCT-1999;
Location/Qualifiers
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Sequence 18 from patent US 5962267.
AR077834.1 GI:10004580
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6 BA3309
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A112514
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AR275652
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SYNINSGS
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AR134709
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-MODEL=frame+ pan.model -DEV=xlp
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AX107018 Sequence
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AX179492 Sequence
                                                                                                                       October 28, 2004, 16:28:53; Search time 721.759 Seconds (without alignments) 720.721 Million cell updates/sec
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                     GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                        OM protein - nucleic search, using frame_plus_p2n model
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hit's satisfying chosen parameters:
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60.0 , Ygapext 60.0
6.0 , Fgapext 7.0
6.0 , Delext 7.0
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AX107018
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Maximum DB seq length: 200000000
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/translation="Werrijplialmgpdpaashlvealylvsgergffytpktr
Ieaeagagsloplalegslokipr"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ben-Nun, A., kerlero de Rosbo, N. and Sappler, G.P. Synthetic human genes and polypeptides and their use in the treatment of autoimmune diseases
Patent: Wo 0.131037-8, 0.3-MAY-2001;
YEDA RESEARCH AND DEVELOPMENT CO. LTD. (IL)
Location/Qualifiers
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Sequence 6 from Patent US 4801536.
101821
101821.1 GI:269797
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Sequence 87 from Patent W00131037.
AX179492. GI:14599120
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Pred. No.:
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AX179492
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VO1461.02546

VO1461.02546

VO1461.1 G1:88303

Strifficial gene; gene synthesis.

Synthetic construct

Synthetic construct

Synthetic construct

Synthetic construct

Synthesis of the human insulin gene. Part III. Chemical synthesis of 5'-phosphomonoester group containing deoxyribooligonucleotides by the modified phosphoritester method. Its application in the synthesis of seventeen fragments constituting human insulin constituting human insulin C-chain
                                                                                                                                  PAT 30-APR-2001
                                                                                                                                                                                                                                                                          Habermann, P., Ertl, J., Meiwes, J. and Seipke, G.
C-peptide for the improved production of insulin and insulin analogues
Patent: WO 0125278-A 1 12-APR-2001;
Aventis Pharma Deutschland GmbH (DE)
                                                                                                                                                                                                                                                                                                                                                                          1 .87
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                                  GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
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Sequence 1 from Patent W00125278.
AX107018
AX107018.1 GI:13922551
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   US-10-783-095-9 (1-11) x AR077834 (1-68)
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artificial sequences.
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Title: Perfect :

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Adc51568 Human pro-
Adf16306 Human alb
Adh17810 Optimised
Aar17831 Optimised
Aar17830 Human lon
Aar15830 Human lon
Aar45975 Gene for
Aar45975 Gene for
Aar45975 Gene for
Aar67355 Merryy hu
Aar870072 Sequence
Aar37003 Proinsuli
Aar38310 hpI gene.
Aar37003 Proinsuli
Aar38310 hpI gene.
Aar38310 hpI man mRN
Aar38310 hpI man ins
Aar58210 Human ins
Aar5821 Human ins
Aar5821 Human ins
Aar5831 Human ins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR primer used to produce chimeric genes of the invention.
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AAT17831
AAT17830
AAT17830
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AAN50152
AAN505208
AAN5652
          AAT37134
ADC51568
ADF16306
ADH21708
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ALEX-) ALEXION PHARM INC. (MUEL/) MUELLER J P. (MATI/) MATIS L A.
 Synthetic.
Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO9932136-A1.
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AAX86082/c
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-DB=N Geneseq_238ep04 - OFMN=fastap -SUPFIX=oli.rng -MNINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 - UNITS=bits -STRAT=1 - END=-1 -MATRIX=oligo - TRANS=human40.cdi
-LIST=45 - DCCALIGN=200 - THR SCORE-quality - THR MINI=1 - ALIGN=15 - MODE=LOCAL
-OUTFWT=pto - NORM=ext - HEAPBIZE=500 - MINIEN=0 - MAXIEN=200000000
-USER=USI0783095_GCGN 1 1_1241_@runat_2 2610204_18545_4 25024 - NOFU=6 - ICPU=3
-NO WMAP - LARGEGUERY -NBG-SCORES=0 - WAIT - DSPBICCK=100 - LONGLOG
-DBV TIMBOUT=120 - WARN TIMBOUT=30 - THRRAD=2 - TAGAPOP=60 - KGAPOP=6
-DBV TIMBOUT=120 - WARN TIMBOUT=30 - THRRAD=2 - TELEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aax86082 PCR prime
Aaf61522 Human pro
Aat45977 Oligonucl
Aat45973 DNA encod
Aat45974 DNA encod
Aas04793 Synthetio
                                                                               October 28, 2004, 16:24:37; Search time 143.265 Seconds (without alignments) 403.055 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                          nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                         4134886 segs, 2624710521 residues
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                                                                                                                                                                                          5 60.0 , Xgapext 60.0
5 60.0 , Ygapext 60.0
5 6.0 , Fgapext 7.0
6.0 , Delext 7.0
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AAF61522
AAT45977
AAT45973
AAT45974
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Geneseqn1980s:*

Geneseqn2000s:*

Geneseqn2001as:*

Geneseqn2001as:*

Geneseqn2001as:*

Geneseqn2001as:*

Geneseqn2003as:*

Geneseqn2003as:*

Geneseqn2003as:*
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geneseqn2003ds:*
geneseqn2004s:*
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Maximum DB seq length: 200000000
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201
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Ygapop
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Match
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Database :

Score

Result 8

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44444

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The specification describes chimeric fusion proteins comprising immunodominant epitopes of glutamate decarboxylase (GAD) and insulin. The chimeric fusion proteins comprises insulin chain B and individual peptide moieties consisting of at least one GAD65 peptide capable of eliciting a human T cell response, where the insulin chain B and GAD65 peptide are covalently linked and the chimeric fusion protein is capable of eliciting covalently linked and the chimeric fusion proteins are used to treat parients that are predicted to be at risk of developing Type I diabetes one GAD65 peptides. The chimeric fusion proteins are used to treat parients that are predicted to be at risk of developing Type I diabetes and those suffering from Type I diabetes. The fusion proteins can also be used to diagnose patients suffering from insulin dependent diabetes mellitus (IDDM) and/or Stiff Man syndrome. This is also useful for determining the suitability of patients as recipients of transplants of pancreatic cells or tissues. The present sequence represents a primer used to construct genes encoding the chimeric fusion proteins of the
                                                                                                             Chimeric fusion proteins comprising immunodominant epitopes of glutamate decarboxylase and insulin, used to treat patients that have or are predicted to be at risk of developing Type I diabetes.
                                                                                                                                                                                                                                 Example; Page 62; 67pp; English
Mueller JP, Matis LA,
                                                         WPI; 1999-405113/34.
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Sequence 66 BP; 10 A; 27 C; 21 G; 8 T; 0 U; 0 Other;

0.00155 Length: 11.00 Matches: 100.00\$ Conservative: 100.00\$ Mismatches: 2 Gaps:
0.00155 11.00 100.00% 100.00%

US-10-783-095-9 (1-11) x AAX86082 (1-66)

AAF61522 standard; DNA; 87 AAF61522; AAP61522 1D AAP61522 XX XX XX DDT 04-1 DD 04-1 DD 06-1 DD 06-1

(first entry) 04-JUL-2001 Human proinsulin C-peptide encoding DNA.

ds. Insulin; proinsulin; C-peptide; human; B-chain; A-chain; diabetes;

Homo sapiens.

DE19947456-A1

05-APR-2001

02-OCT-1999;

99DE-01047456

99DE-01047456 02-OCT-1999;

Seipke G; Meiwes J, (AVET) AVENTIS PHARMA DEUT GMBH Ertl J, Habermann P,

2001-267042/28.

P-PSDB; AAB70847

New synthetic derivatives of the C-peptide of proinsulin, useful in the

Example 7; Page 15; 22pp; English.

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This invention describes novel synthetic derivatives (I) of the C-peptide of proinsulin. Such novel derivatives of human insulin or insulin analogs represented by (I) are of formula Fus-8(1:30) - RDVP-YN-A(1:21). Fus a optionally present fusion component of arbitrary sequence; B(1:30) = the C-terminal; n = 2-50 (defining the chain length of Y), and A(1:21) at the C-terminal; n = 2-50 (defining the chain length of Y), and A(1:21) at the A-chain of human insulin; the A- and/or B-chain(B) may be modified by amino acid exchanges, additions and/or B-chain(B) may be modified by amino acid exchanges, additions and/or B-chain(B) may be modified by amino acid exchanges, additions and/or B-chain(B) may be modified by intermediates for human insulin or its analogs, which are used in the treatment of diabetes. A claimed method of preparing human insulin (or analogs) involves preparing (I), folding (I) so that disulfide bonds as in human insulin can form, enzymatically removing the RDVP-Yn part and can be prepared in increased around 20% compared with that obtained using plasmid plum730d. The control of enzymatic procession gis also improved. The folding rate is comparable with that obtained using simian prepronnent encoded by plum70d. This sequence encodes the human proinsulin C-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Single chain insulin polypeptide(s) - used for treating diabetes.
preparation of human insulin or insulin analogs in high yield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Miller AR;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 87 BP; 10 A; 27 C; 37 G; 13 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0000
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                                                                                                                                                                                                                                                                                                                                                                                           which is described in the method of the invention
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Matches:
Conservative:
Mismatches:
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                                    Disclosure; Page 7; 12pp; German.
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95US-00435762
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100.00%
100.00%
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Best Local Similarity:
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05-MAY-1995;
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Sequence 12, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 1, Appli
Sequence 1, Appli
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Sequence 7, Appli
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Sequence 7, Appli
Sequence 1, Appli
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Sequence 9, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 11, Appli
Sequence 11, Appli
Sequence 11, Appli
                                       Sequence 41, Appl
Sequence 42, Appl
Sequence 28, Appl
Sequence 12, Appl
Sequence 1, Appli
Sequence 1, Appli
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Patent No. 5962267
GENERAL INFORMATION:
APPLICANT: SHIN, Hang Cheol
APPLICANT: KIN, Dae Young
APPLICANT: KIN, Dae Young
APPLICANT: KIN, Chong Suhl
TITLE OF INVENTION: for Producing Human Insulin
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHIN, Hang Cheol
STREET: Sangma-Hanshin Apt. 102-1206,
STREET: Sangma-Hanshin Apt. 102-1206,
STREET: Strungki-do
COUNTRY: Republic of Korea
COUNTRY: Republic of Korea
STREET: Hyundai Apt. 71-203, Apkujong-dong,
STREET: Hyundai Apt. 71-203, Apkujong-dong,
STREET: Kangmam-ku
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: KIM, Dae Young
STREET: Sosa Jukong Apt. 108-202, Sosa Bon-dong,
STREET: Sosa-ku
                                    US-08-033-731A-41
US-08-030-731A-42
US-08-030-731A-42
US-07-696-551B-12
PCT-US-5-701-1
US-09-280-030-64
US-08-580-63
US-08-580-63
US-08-580-030-48
US-08-78-271-3
US-08-78-271-3
US-08-185-852-1
US-09-185-852-1
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Garden Heights Apt. 202-801, #100,
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US-09-485-286-9
US-09-485-286-14
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US-09-537-696-12
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US-08-081-661-3
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STATE: Kyungki-do
COUNTRY: Republic of Korea
ZIP: 422-230
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Seoul
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STREET: Ga
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  Sequence 18, App
Sequence 1, Appl
                                                                                     October 28, 2004, 20:02:28; Search time 32.6024 Seconds (without alignments) 239.819 Million cell updates/sec
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3: /cgn2_6/ptodateall/ina/6A_COMB.seq:*
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5: /cgn2_6/ptodateall/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodateall/ina/PcTUS_COMB.seq:*
           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                               nucleic search, using frame_plus_p2n model
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US-09-676-787-1
US-08-673-312-10
US-07-918-953-12
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US-07-918-953-14
US-07-918-953-14
US-07-918-953-16
US-07-918-953-16
US-07-715-183C-3
US-07-715-183C-3
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), Ygapext 60.0
), Fgapext 7.0
), Delext 7.0
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Maximum DB seq length: 2000000000
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GENERAL INFORMATION:
APPLICANT: SHIN, Hang Checl
APPLICANT: CHANG, Seung Gu
APPLICANT: KIM, Dae Young
APPLICANT: KIM, Chong Suhl
TITLE OF INVENTION: Proinsulin Derivative and Process
TITLE OF INVENTION: for Producing Human Insulin
NUMBER OF SEQUENCES: 36
CORRESPONDENCE 36
CORRESPONDENCE ADDRESS:
ADDRESSE: SHIN, Hang Checl
STREET: Stangma-Hanshin Apt. 102-1206,
CITY: Kwangmyung-shi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Taeyu
STATE: Taegu
COUNTRY: Republic of Korea
ZIP: 706-04
MEDUW TYPE: Ploppy Disk, 3.5 inch, 1.44MB storage
COMPUTER READABLE FORM:
MEDUW TYPE: Ploppy Disk, 3.5 inch, 1.44MB storage
COMPUTER: ISH PC/AT
OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/600,783
FILING DATE:
** APPLICATION: 514
** TASIFICATION: 514
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ZIP: 1135-110
ADDRESSBE: KIM, Dae Young
STREET: Sosa Jukong Apt. 108-202, Sosa Bon-dong,
eTREET: Sosa-ku
Matches:
Conservative:
Mismatches:
Indels:
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COUNTRY: Republic of Korea
ZIP: 423-030
ADDRESSEE: CHANG, Seung Gu
STREET: Hyundal Apt. 71-203, Apkujong-dong,
STREET: Kangnam-ku
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ADDRESSEE: KIM, Chong Suhl
STREET: Garden Heights Apt. 202-801, #100,
STREET: Hwangkeum-dong, Soosung-ku
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PRICA APPLICATION DATA:
APPLICATION NUMBER: KR 95-2751
FILING DATE: 15-FEB-1995
ATTORNEY/AGRET INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
                                                                                                                                                                                                                                                                                                                                                                                                  US-08-600-783-17; Sequence 17, Application US/08600783; Patent No. 5962267
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-1000
TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO: 17:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Kyungki-do
COUNTRY: Republic of Korea
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Query Match:
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APPLICANT: HABERMAIN, Paul
APPLICANT: HABERMAIN, Paul
APPLICANT: ERIL, Johannes
APPLICANT: ERIL, Johannes
APPLICANT: SEIPKE, Gerhard
TITLE OF INNENTION: C REPTIDE FOR IMPROVED PREPARATION OF INSULIN ANALOGS
FILE REFERENCE: 38005-0110
CURRENT APPLICATION NUMBER: US/09/676,78,7
CURRENT FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NOS: 87
                                                          STATE: Taegu
COUNTRY: Republic of Korea
ZIP: 706-040
ZIP: 706-040
COMPUTER: Republic form:
MEDIUM TYPE: Floppy Disk, 3.5 inch, 1.44MB storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,783
FILING DATE:
CLASSIFICATION DATA:
APPLICATION NUMBER: KR 95-2751
FILING DATE: 15-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER:
TELECOMMUNICATION INFORMATION:
THE CONTRACTION NUMBER:
TELECOMMUNICATION INFORMATION:
THE CONTRACTION NUMBER:
TELECOMMUNICATION INFORMATION:
THE CONTRACTION INFORMATION INFORMATION:
THE CONTRACTION INFORMATION INFORMATION
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Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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            Hwangkeum-dong, Soosung-ku
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; Sequence 1, Application US/09676787
; Patent No. 6534288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (212) 278-1000
TELEPAX: (212) 253-7249
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.000207
11.00
100.00%
100.00%
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TYPE: nucleic acid
STRANDEDNESS: single
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; ORGANISM: Homo sapiens
US-09-676-787-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ANTI-SENSE: yes
US-08-600-783-18
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            STREET: Hwa:
CITY: Taegu
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Sequence 43, Appl
Sequence 43, Appl
Sequence 27, Appl
Sequence 1, Appl
Sequence 1, Appli
Sequence 44, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 43, Appl
Sequence 42, Appl
Sequence 7, Appl
Sequence 9, Appl
Sequence 25, Appl
Sequence 25, Appl
Sequence 14, Appl
                                                                    Sequence 17, Appl
Sequence 23, Appl
Sequence 21, Appl
Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 4, Appli
Sequence 4, Appli
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPI
APPI
APPI
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APPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 1388, Åp
                                                                                                                                             Sequence 49, Ar
Sequence 48, Ar
Sequence 5, Ar
Sequence 1, Ap
Sequence 43, A
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Sequence 32, 1
Sequence 42, 1
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Sequence 43,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 47,
Sequence 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 31,
                                    5 US-10-383-285-1

0 US-09-807-742-16

0 US-09-807-742-16

0 US-09-807-742-16

0 US-09-807-742-17

1 US-10-346-142-21

5 US-10-346-173-1

1 US-09-280-033-49

2 US-10-411-032-43

2 US-10-411-097-43

1 US-10-411-097-43

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5 US-10-411-012-43

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7 US-10-411-012-43

7 US-10-411-012-43

8 US-10-609-019-42

8 US-10-609-019-42

8 US-10-430-752A-7

8 US-10-430-752A-7

8 US-10-430-752A-7

8 US-10-430-752A-7

8 US-10-430-752A-7

8 US-10-609-019-43

8 US-10-609-019-43

8 US-10-613-032-13

8 US-10-613-032-13

8 US-10-419-539-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
              Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11255
11271
11332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
CRGANISM: Homo sapiens
US-10-383-285-1
Query
Match
                                         RESULT 1
US-10-383-285-1
              Score
                                                                                                                                                              Result
              No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      October 28, 2004, 22:07:29 ; Search time 580.217 Seconds (without alignments) 97.211 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Published Applications NA:*

1. (cgn2_6/ptodata/1/Pubpna/US07_PUBCOMB.seq:*
2. (cgn2_6/ptodata/1/Pubpna/PCT_NEW_PUB.seq:*
3. (cgn2_6/ptodata/1/Pubpna/US06_NEW_PUB.seq:*
4. (cgn2_6/ptodata/1/Pubpna/US06_PUBCOMB.seq:*
5. (cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*
6. (cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*
7. (cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*
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9. (cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*
10. (cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*
11. (cgn2_6/ptodata/1/Pubpna/US08_NEW_PUB.seq:*
12. (cgn2_6/ptodata/1/Pubpna/US08_PUBCOMB.seq:*
13. (cgn2_6/ptodata/1/Pubpna/US08_PUBCOMB.seq:*
14. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
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17. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
18. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
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19. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
10. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
10. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
12. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
13. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
14. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
15. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
16. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
17. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
18. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
19. (cgn2_6/ptodata/1/Pubpna/US10A_PUBCOMB.seq:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                    - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                              residues
                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
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Post-processing: Listing first 45 summaries

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

60.0 60.0 7.0

60.0 , Ygapext 6 , 60.0 , Ygapext 6 , 6.0 , Fgapext 6.0 , Delext

Xgapop (Ygapop (Fgapop Delop OFIGO

1 QPLALEGSLOK 11 US-10-783-095-9

Title: Perfect score:

Sequence:

OM protein

Run on:

Scoring table:

3413475 segs, 2563800928

Word size:

Searched:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

80 .	FINS IN TRANSGENIC	260 0 0 0		PROTEINS IN TRANSGENIC	
Length: 258 Matches: 11 Conservative: 0 Mismatches: 0 Indels: 0 Gaps: 0 1 (1-258)	Ħ	h: nes: ervative: atches: ls: :		TICAL al Sec	
-285- -285- 	09807742 4A1 ICN OF PHARM 100 100 100 100 100 100 100 10	07-742-	(nC)	ion US/09807742 30204864A1 HENRY PRODUCTION OF PHARMACEUTIC PLASTIDS PLASTIDS OOL 04-18 MNBER: DC7/US01/06288 0001-02-28 3: 19 ler. 2.1 Description of Artificial modified proinsulin seques	
0.00302 11.00 11.00 10.00\$ 100.00\$ 15 15 -11) x US-10-383 16	ication US/ \$22003020486 ON: HENRY ON: PRODUCT ON: PLASTII 1465-PCT-US ION NUMBER: 12001-02- N NUMBER: PE: 2001- N NUMBER: PE: 2001- IN VET: 2.1	0.0 11: 100 100 100 10	oreualareu TTGGCCTG	cation US/098 220030204864A1 N: HENRY N: PEROTION N: PLASTIDS (465-PCT-US-00 (465	
ment Scor No.: It Simila Local Sim Match: -783-095-	2 807-742- ence 16, ication CRAL INFO CRAL INFO CE OF IN EE REFEREE RENT APPEL OR FILIN OR OR FILIN OR FILIN OR FILIN OR FILIN OR FILIN OR FILIN OR FILIN OR	nment Scores: . No.: s: ent Similarity Local Similar / Match:	1 160	RESULT 3 US-09-807-742-17 Sequence 17, Application US/09807742 Publication No. US20030204864A1 GENERAL INFORMATION: APPLICANT: DANTELL, HENRY TITLE OF INVENTION: PLASTIDS FILE REFRENCE: 1465-PCT-US-00 CURRENT FILING DATE: 2001-04-18 PRIOR APPLICATION NUMBER: US/09/807,742 CURRENT FILING DATE: 2001-04-18 PRIOR APPLICATION NUMBER: PCT/US01/06288 PRIOR FILING DATE: 2001-02-28 NUMBER OF SEQ ID NOS: 19 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 17 LENGTH: 260 TYPE: DNA CORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: modified proinsulin seq. US-09-807-742-17	
Align Prede Score Perce Best Query DB: US-10	RESULT US-091-1 Seque RESULT FULL RESULT RES	Align Pred. Score Perce Best Query DB:	qq Xo	RESULT OS-09-1 PUDD ORNE TITIT TITIT PRICE SOF SOF SOF SOF SOF SOF SOF SOF	

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RESULT 4

RESULT 6

RESULT
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Matches:
Conservative:
Mismatches:
Indels:
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                    Length:
Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-783-095-9 (1-11) x US-10-746-149-23 (1-260)
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US-10-609-019-21
Sequence 21, Application US/10609019
Publication No. US20040197910A1
GENERAL INFORMATION:
APPLICANT: Cooper, Richard K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
CTHER INFORMATION: Synthetic
US-10-746-149-23
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Best Local Similarity:
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DB:
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Best Local Similarity:
Query Match:
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Alignment Scores:
Pred. No.:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - pr	OM protein - protein search, using sw model
Run on:	October 28, 2004, 11:13:10 ; Search time 5.6988 Seconds (without alignments) 185.721 Million cell updates/sec
Title:	US-10-783-095-9
Sequence:	1 OPLALEGSLOK 11
Scoring table:	OLIGO Gapop 60.0 , Gapext 60.0
Searched:	283416 segs, 96216763 residues
Word size .	

Post-processing: Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description					insulin precursor	hypothetical prote		insulin precursor	glutamine-fructose	а			SOJ protein (soj)	_	Ψ	movement protein -	probable transport	hypothetical prote	enoyl-[acyl-carrie	enoyl-acyl carrier	hypothetical prote	porphobilinogen de	o-sialoglycoprotei	O-sialoglycoprotei	probable Transposa	deoxyhypusine synt	14	probable FAD-depen	probable indole-3-
SUMMARIES	D	IPHU	B42179	JQ0178	~	IPDG	T40386		IPGP	PC4141	T46419	A75571	H64230	H90142	B85065	800008	\$65054	S48700	E90194	C64544	B71964	8379	25	7210	651	9589	E22	59	8299	0058
	DB	-	~	N	N	Н	Ŋ	Ŋ	н	N	Ŋ	N	2	Ŋ	~	N	(1)	~	2	2	0	7	7	~	~	N	~	~	~	7
	Length		н	110	ч	Н	S	80	Н	S	9	0	Ч	S	3	3	9	9	272	7	7	ΟJ	2	4	4	ın	ω	œ	0	4
ن	Query Match			100.0																										
	Score	11	11	11	11	7	7	9	9	9	9	ę	9	9	9	ω	φ	9	9	9	9	9	9	9	9	9	9	9	9	9
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indole-3-acetate b	intermediate filam	hydrogenase-4 comp	hydrogenase 4 memb	hydrogenase 4 memb	thiazole biosynthe	NADH2 dehydrogenas	n-acetylglucosamin	ATP-dependent RNA	conserved hypothet	atp dependent heli	glutamine-fructose	glutamine-fructose	glutamine-fructose	glutamine-fructose	hypothetical prote
T00584	A56600	C65024	B91047	F85891	F83005	T12401	559642	G95184	G98051	T41007	H71809	D64711	C81281	C97575	AC2796
(1)	N	~	2	7	7	7	N	0	N	N	0	~	N	~	N
455	464	479	479	479	484	495	518	524	524	595	597	597	298	608	608
54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5	54.5
vo	w	œ	w	ø	w	ø	ø	ø	Q	w	ø	ø	Q	v	w
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

283416

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

IPHU
insulin precursor [validated] - human
N;Alternate names: preproinsulin
C;Species: Homo sapiens (man)
C;Date: 23-Oct-1981 #sequence revision 23-Oct-1981 #text change 09-Jul-2004
C; Accession: A93222; A94253; A93216; A94251; A93144; A92075; A91186; I58114; A015
R;Bell, G.I.; Pictet, R.L.; Rutter, W.J.; Cordell, B.; Tischer, E.; Goodman, H.M.
Nature 284, 26-32, 1980
A, Title: Sequence of the human insulin gene.
A;Reference_number: A93222; MUID:80120725; PMID:6243748
A; Accession: A93222
A; Molecule type: DNA

579; \$58

A;Residues: 1-110 cBEL>
A;Residues: 1-110 cBEL>
A;Residues: 1-110 cBEL>
A;Residues: 1-110 cBEL>
A;Cross-references: UNIPROCT:P01308; GB:J000265; NID:g186429; PIDN:AAA59172.1; PID:g386828
R;JJItich, A.; Dull, T.J.; Gray, A.; Broslus, J.; Sures, I.
A;Atle: Genetic variation in the human insulin gene.
A;Reference number: A94253; MUID:80236313; PMID:6248962
A;Accession: A94253; MUID:80236313; PMID:6248962
A;Residues: 1.10 cULL>
A;Residues: 1.10 cULL>
A;Residues: 1.10 cULL>
A;Residues: 1.10 cult.
A;Residues: 1.10 cand.
A;Reference number: A93216; MUID:8054779; PMID:50334
A;Molecule type: mRNA
A;Residues: 1.10 cand.
A;Reference number: A94251; MUID:80147417; PMID:6927840
A;Title: Nucleotide sequence of human preproinsulin complementary DNA.
A;Residues: 1.10 cand.
A;Reference number: A94251; MUID:80147417; PMID:6927840
A;Atle: Nucleotide sequence of human insulin.
A;Reference number: A94251
A;Molecule type: mRNA
A;Residues: 1.10 cand.
A;Reference number: A94251
A;Molecule type: mRNA
A;Residues: 1.10 cand.
A;Reference number: A94251
A;Ancesidues: L10 cand.
A;Reference number: A94251
A;Ancesidues: Call.
A;Atle: Amino-acid sequence of human insulin.
A;Atle: Amino-acid sequence of human insulin.
A;Atle: Amino-acid sequence of human insulin.
A;Atle: Anino-acid sequence of human insulin.
A;Atle: Anino-acid sequence of human insulin.
A;Atle: Anino-acid sequence of human insulin.

A,Molecule type: protein
A,Residues: 25-54;90-110 <NIC>
R,Residues: 25-54;90-110 <NIC>
R;Oyer, D.E.; Cho, S.; Peterson, J.D.; Steiner, D.F.
A;D Biol. Chem. 246, 1375-1386, 1971
A;Title: Studies on human proinsulin. Isolation and amino acid sequence of the human pan A;Reference number: A92075; MUID:71116410; PMID:5101771
A;Accession: A92075
A;Molecule type: protein

N

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A/Cross-references: UNIPROT: P30407; EMBL: X61092; NID: g22808; PIDN: CAA43405.1; PID: g22809 A/Cross-references: UNIPROT: P30407; EMBL: X61092; NID: g5185, NCBIP: 95194)
R. Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Biol. Chem. 247, 4866-4871, 1972
A;Title: Determination of the amino acid sequence of the monkey, sheep, and dog proinsuling Reference number: A92111; MUID: 72258016; PMID: 4626369
A) Rocession: A05232
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R;Weterkam, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
R;Weterkam, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
A;Title: The nucleotide sequence of cDNA coding for preproinsulin from the primate Macaca
A;Reference number: JQ0178; MUID:83080474; PMID:6184262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            insulin precursor - chimpanzee
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42179; S22058
R;Seino, S.; Bell, G.I.; Li, W.H.
Mol. Biol. Evol. 9, 193-203, 1992
A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of A;Reference number: A42179; MUID:92219953; PMID:1560757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           insulin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .Introns: 63/1.
.Superfamily: insulin
.Yeywords: hormone; pancreas
.1-24/Domain: signal sequence #status predicted <SIG>
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Matches 11; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 57-87 <PET>
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A; Residues: 1-110 <WET>
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R;Sleber, P.; Kamber, B.; Hartmann, A.; Joehl, A.; Riniker, B.; Rittel, W.
R;Sleber, P.; Kamber, B.; Hartmann, A.; Joehl, A.; Riniker, B.; Rittel, W.
A;Title: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindungen.
A;Reference number: A91636; MUID:75077277; PMID:4443293
A;Contents: annotation; synthesis
A;Note: aisulfide-bonded human insulin was synthesized; the synthetic hormone was identi
A;Note: article in German with English abstract
R;Naithani, V.K.
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A;Title: The synthesis of C-peptide of human proinsulin.
A;Reference number: A91658; MUID:75040007; PMID:4803504
A;Contents: annotation; synthesis of residues 57-87
B;Getger, R.; Jaeger, G.; Koenig, W.
Chem. Ber. 106, 2347-2352, 1973
A;Title: Synthesis of the complete sequence of human proinsulin C-peptide and its [Glu-9
                                                                                                                                                                                                                                                A;Wolecule type: protein
A;Residues: 57-87 cx0x,
R;Jucassen, A.M.; Julier, C.; Beressi, J.P.; Boitard, C.; Froguel, P.; Lathrop, M.; Bell
Nature Genet. 4, 305-310, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A, Reference number: A90914

A, Reference number: A90914

R, Contents: annotation, synthesis of residues 57-87

R, Kaufmann, J.E.; Irminger, J.C.; Halban, P.A.

Biochem. J. 310, 869-874, 1995

A, Reference number: S58661; MUID: 96013185; PMID: 7575420

A, Contents: annotation; site-directed mutagenesis study of proteolytic processing
                                                                                                                                                                                                                                                                                                                                                                                        A,Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment A,Reference number: 158114; MUID:93364428; PMID:8358440
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C;Species: Cercopithecus acthiops (green monkey, grivet)
C;Species: Cercopithecus acthiops (green monkey, grivet)
C;Accession: B42179; A05232; Sī4644; S22056
R;Scino, S.; Bell, G.I.; Li, W.H.
Mol. Biol. Evol. 9, 193-203, 1992
A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of A;Reference number: A42179; MUID:92219953; PMID:1560757
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                                                                  ;Ko, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
ur. J. Blochem. 20, 190-199, 197.
Title: Amino acid sequence of the C-peptide of human proinsulin.
;Reference number: A91186; MUID:71257722; PMID:5560404
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C;Keywords: hormone; pancreas
E;1-24,Domain: signal sequence #status predicted <SIG>
F;1-24,Domain: signal sequence #status experimental <BCH>
F;25-54,90-110/Product: insulin that #status experimental <MAT>
F;25-54,90-110/Product: insulin #status experimental <MAT>
F;7-87/Domain: connecting C peptide #status experimental <CPE>
F;90-110/Domain: insulin chain A #status experimental <ACH>
F;31-96,43-109,95-100/Disulfide bonds: #status experimental
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A;Molecule type: DNA
A;Residues: 1-59,63-110 <RES>
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A;Map position: 11p15.5-11p15.5
A;Introns: 63/1
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A;Residues: 57-87 <OYE>
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BQ267254
ikOlbO7.yl Human insulinoma Homo sapiens CDNA clone IMAGE:5779548
5' similar to SW:INS_HUMAN P01308 INSULIN PRECURSOR. [1] ;, mRNA
BQ272395 ij98c08.x
BQ48611 ij98c08.x
BQ48672 ij45c11.x
BQ586701.x
BQ267401 ik92b08.x
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BW657401 ik06f01.x
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1 (bases 1 to 118)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Emdozinia Pancreas Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Bravard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@blobp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining
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Homo sapiens
           sequence.
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   BQ267254 ikolbo7.y
BQ272508 ikolbo7.x
BU073408 im35e06.x
BI066839 ic59808.x
BI466930 ic60910.x
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JOURNAL
COMMENT
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AUTHORS
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                                                                           FEATURES
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                                                                                                                 /uradian="Homo sapiens"
// mol type="mRNA"
// mol type="mRNA"
// db_xef="lavan:9666"
// clone="InAGE:5779548"
// lab_host="Hulba"
// lab_host="Hulba"
// lab_host="Hulba"
// lab_host="Hulba"
// lab_host="lab|10B (phage-resistant)"
// lab_host="lab|10B (phage-resistant)"
// clone lib="Human insulinoma"
// clone lib="Human insulinoma"
// clone lib="Human insulinoma"
// clone lib="Human insulinoma"
// clone lib="Corgi; Constructed with lambda ZAPII system
// Stratagene) by Dr. H. Incue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Mashington University School of Medicine, Box
8127, 660 & Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas BST project library. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (Dases 1 to 118)

S. (Dases 1.0 118)

S. Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Bistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.

Endocrine Pancreas Consortium

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue Endocrine Pancreas Consortium

Bradocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute

Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BQ272508 ikOlb07.xl Human insulinoma Homo sapiens cDNA clone IMAGE:5779548 3' similar to SW:INS_HUMAN P01308 INSULIN PRECURSOR. [1] ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
                        Possible reversed clone: similarity on wrong strand Seg primer: -40RP from Gibco. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
Conservative:
Mismatches:
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
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EST.
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                                                                           FEATURES
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DRIGIN

Score:

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/organism="Homo sapiens"

//organism="Homo sapiens"

//organism="Homo sapiens"

//db = "maxon:9606"

//db = "InAGE:5779548"

//db host="DilloB (phage-resistant)"

//dloce="Organ: pancreas; Vector: pBluescript SK-; Site_1:

//dloce="Organ: pancreas; Vector: pBluescript SK-; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (http://genome.wustl.edu/est/lambda_protocol.shtml).
Please contact Hiroshi Inoue, MD/PhD for further
Information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Bullid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
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Library was constructed by Dr. J. Ferrer In vivo mass-excised to
Library was constructed by Dr. J. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining a
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
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I. (Bases I to 118)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Fillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
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Endocrine Pancreas Consortium
Barvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
                                                   Possible reversed clone: similarity on wrong strand
Seg primer: -400P from Gibco.
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Unpublished (2000)
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Sun Oct 31 14:58:46 2004

us-10-/83-095-9.011.rup

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

- protein search, using sw model OM protein

October 28, 2004, 10:57:30; Search time 27.8313 Seconds (without alignments) 227.410 Million cell updates/sec Run on:

US-10-783-095-9 11 1 OPLALEGSLOK 11 Title: Perfect score: Sequence:

Scoring table:

OLIGO Gapop 60.0 , Gapext 60.0

1825181 segs, 575374646 residues Searched:

0 Word size :

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		% Query				
¦	Score	Match	l Length	a ¦	1D	Describtion
_	11		9	7	Q8HZ80	8hz80
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ALIGNMENTS

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	PRT;				Last			а;					O'huigin C., Tichy H., Klein J.;	EMBL	·	C:extracellular; IEA.	F:hormone activity; IEA.	GO; GO: 0007582; P:physiological process;	F/rel						0		
	۲¥ ;			l. 23,			tan).	Chordata;	Primates;				, Klei	to the	AAM76641.1;	racell	none a	siolog	Ins/IG	1, 1.		10	6920 MW;	100.0%;	i ve	11	28
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	0	.;0	01-MAR-2003	01-MAR-2003	01-MAR-2004	Insulin (Fragment).	Pongo pygmaeus (Orangutan).	Eukaryota; Metazoa;	Mammalia; Eutheria;	NCBI TaxID=9600;		SEQUENCE FROM N.A.	gin C.	tted (EMBL; AY092024;	GO:0005576;	GO:0005179;	0:0001	Pro; I	Pfam; PF00049; Insulin; 1.	ER	ER	NCE	Query Match Best Local Similarity	11;	1	48 05
H C	QSHZ80	Q8HZ80;	01-MAJ	01-MA	01-MA	Insul	Pongo	Eukar	Матта	NCBI	Ξ	SEQUE	o'hui	Submi	EMBL;	9 9	g G	8 9	Inter	Pfam;	NON TER	NON TER	SEQUENCE	Query Match Best Local	Matches		
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OSHZ81 PRELIMINARY, PRT, 65 AA.

OSHZ81;
OLI-MAR-2003 (TrEMBLrel. 23, Created)
OL-MAR-2003 (TrEMBLrel. 24, Last sequence update)
OL-MAR-2003 (TremBLrel. 24, Last annotation update)
OL-UN-2003 (TremBLrel. 24, Last annotation update)
Insulin (Fragment).
Gorilla Gorilla (Gorilla).
Eukaryota, Metazoa; Chordata, Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla. RESULT 2 Q8HZ81 DT ACCOUNT THE BEAUTH OF THE B

[1] SEQUENCE FROM N.A. G. Alein J.; SEQUENCE FROM N.A. O'NUIGIN C., Tichy H., Klein J.; GenBank/DDBJ databases. L. SEMEELLULAR LOCATION: Secreted (By similarity). Series of the insulin family. Belongs to the insulin family. Belongs to the insulin family.

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Gaps

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Matches

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100.0%; Score 11; DB 1; Length 110; 100.0%; Pred. No. 0.0016; Pred. No. 0. 100.0%; ive 0; Mismatches 0; Indels
                                                                                  24 Insulin B chain.
54 C peptide.
110 Insulin A chain.
96 Interchain.
109 Interchain.
100
110 MW, 95AIF54BE7B247F9 CRC64;
Direct protein sequencing; Glucose metabolism; Hormone; SIGNNI, family; Signal.
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Best Local Similarity 100.
Matches 11, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=9221953; PubMed=1560757; MEDLINE=921953; PubMed=1560757; Seino S., Bell G.I., Li W.; Seino S., Bell G.I., Li W.; "Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys."; Mol. Biol. Evol. 9:193-203(1992).
                                                                                                                                                                                                                                                                                                                         Gaps
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J. Biol. Chem. 247:4866-4871(1972).
J. Biol. Chem. 247:4866-4871(1972).
J. Biol. Chem. 247:4866-4871(1972).
J. FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.

SUBUNIT: Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=72258016; PubMed=4626369; electron 0.10., Nehrlich S., Oyer P.E., Steiner D.F.; electron 0.10., Nehrlich S., Oyer P.E., Steiner D.F.; electron 0.10., Nehrlich S., Oyer P.E., Steiner D.F.; deep, and "Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                     100.0%; Score 11; DB 2; Length 65; 100.0%; Pred. No. 0.001; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                 65 65
65 AA; 6920 MW; B772017FD8BCABEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disulfide bonds.
--- SUBCELLULAR LOCATION: Secreted.
--- SIMILARITY: Belongs to the insulin family.
     GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0007582; P:physiological process; IEA.
InterPro; IPR004825; Ins/IGF/relax.
Pfam; PP00049; Insulin; 1.
Insulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-APR-1993 (Rel. 25, Created)
01-APR-1993 (Rel. 25, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                         100.0%;
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                                                                                                                                                                                                                                                                                                                    11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                    1 OPLALEGSLOK 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 57-87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9534;
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NON TER
SEQUENCE
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"Nucleotide sequence of a cDNA clone encoding human preproinsulin.";
Nature 282:525-527(1979).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93364428; PubMed=8358440;
Lucassen A.M., Bell J.I., Julier C., Lathrop M.;
Susceptibility to insulin dependent diabetes mellitus maps to a 4.
kb segment of DNA spanning the insulin gene and associated VMTR.";
Nat. Genet. 4:305-310(1993).
                                                                                                                                                                                                                                                    Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-80147417; PubMed-6927840; Sures I., Goeddel D.V., Gray A., Ullrich A.; "Nucleotide sequence of human preproinsulin complementary DNA."; Science 208:57-59(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=8054779; PubMed=503234;
Bell G.I., Swain W.F., Pictet R.L., Cordell B., Goodman H.M.,
Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDINES-80120725; PubMed=6243748;
Bell G.I., Pictet R.L., Rutter W.J., Cordell B., Tischer
Goodman H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=80236313; PubMed=6248962;
Ullrich A., Dull T.J., Gray A., Brosius J., Su:
"Genetic variation in the human insulin gene."
Science 209:612-615(1980).
                         21-UUL-1986 (Rel. 01, Created)
21-UUL-1986 (Rel. 01, Last sequence update)
01-0CT-2004 (Rel. 45, Last annotation update)
Insulin precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence of the human insulin gene.";
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RESULT 3

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HSSP, POI308; IAIO.
InterPro; IPRO04035; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
PRINTS; PR00277; INSULINB.
SMART; SM00078; IIGF; I

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LOCATION: 1
) OTHER INFORMATION: AOA-Glu
US-08-105-9048-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Appl
Sequence 10, Appl
Sequence 17, Appl
Sequence 2, Appli
Patent No. 5514646
Sequence 24, Appli
Patent No. 5514646
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Sequence 1, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 1, Appli
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                                                                           (without alignments)
62.550 Million cell updates/sec
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                                                               October 28, 2004, 10:22:24 ; Search time 11.6627 Seconds
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Sequence
Sequence
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/cgn2 6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2 6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd
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US-08-114-877A-10
US-08-537-928-10
US-09-633-269-10
US-09-676-787-2
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US-07-715-183C-1
US-09-477-924-2
US-09-723-896-2
US-09-878-380-1
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US-09-815-229-4
US-09-947-563-3
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US-08-389-487-6
US-09-134-836-3
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US-09-639-667-24
5514646-4
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                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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1 QPLALEGSLQK 11
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Perfect score:
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Appl	4.0	Sequence	US-08-784-582-4	m	110	100.0	23	44
Appla	. 7	Sednence	US-08-784-582-2	т	110	100.0	23	43
Appla	4,	Sednence	US-08-589-028-4	m	110	100.0	23	42
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Appli	σ	Sequence	US-09-701-968-9	4	100	100.0	53	39
App1	œ.	Sequence	US-09-701-968-8	4,	66	100.0	23	38
Appli	,	Seguence	US-09-701-968-7	4	86	100.0	23	3.7
Appl	11	Sequence	US-09-099-307-11	m	97	100.0	53	36
Appli	œ	Sequence	US-09-099-307-8	m	97	100.0	53	35
Appli	۲,	Seguence	US-09-099-307-7	m	97	100.0	23	34
Appli	9	Seguence	US-09-099-307-6	m	76	100.0	53	33
Appli	r.	Sequence	US-08-389-487-7	Н	97	100.0	53	32
Appli	4	Seguence	US-08-160-376A-4	Н	97	100.0	23	31
Appli	'n	Seguence	US-09-947-563-5	4	96	100.0	53	30
Appli	4	Seguence	US-09-947-563-4	4	96	100.0	23	29
Appli	'n	Sequence	US-09-386-303A-5	m	9	100.0	53	28

ALIGNMENTS

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RESULT 1

US-08-105-9049-10

Sequence 10, Application US/08105904B

Patent No. 600154

Patent No. 600154

Patent No. 600154

SEQUENCE 10, APPLICANTON:
PREPARATION:
PREPARATION:
PREPARATION:
PREPARATION:
PREPARATION:
PREPARATION:
PREPARATION:
PREPARATION BY PARALLEL ASSEMBLY
NUMBER OF INVENTION:
PREPARATION BY PARALLEL ASSEMBLY
NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
ADDRESSE:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE:
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSE:
CONTRY: 01.S.A.
ZIP: 3420.Alco Square, 3000 El Camino Real
COUNTRY: 01.S.A.
ZIP: 3420.Alco Square, 3000 El Camino Real
STATE: California
COUNTRY: 01.S.A.
ZIP: SATORE: PatentIn Release #1.0, Version #1.25
COMPUTER: 1BM PC Compatible
OPERATION NUMBER: US/08/105,904B
FILING DATE: 31-AUG-1993
CLASSIFICATION NUMBER: US/08/105,904B
FILING DATE: 31-AUG-1993
CLASSIFICATION NUMBER: US/08/105,904B
FILING DATE: 31-AUG-1993
CLASSIFICATION NUMBER: ABIC-001/02US
FERFERENCE/DOCKET NUMBER: ABIC-001/02US
TELECOMMUNICATION NUMBER: ABIC-001/02US
TELECOMUN
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TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: peptide HYPOTHETICAL: NO
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ORGANISM: Artificial Sequence
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ORGANISM: Artificial Sequence
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Best Local Similarity 100.
Matches 11; Conservative
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US-08-114-877A-10

i Sequence 10. Application US/08114877A

i Sequence 10. Application US/08114877A

j Patent No. 6174530

i APPLICANT: OFFICE No. 6174530

i APPLICANT: Officed, Robin

i TILLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY

ITTLE OF INVENTION: PREPARATION BY PARALLEL ASSEMBLY

NUMBER OF SEQUENCES: 15

CORRESPONDENCE ADDRESS:
                                                  .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
Query Match
100.0%; Score 53; DB 3; Length 23;
Best Local Similarity / 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
STREET: 5 Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/114,877A
FILING DATE: 31.ANG-1993
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/057,594
FILING DATE: 05-MAY-1993
CLASSIFICATION: 424
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Neeley, Richard L.
REGISTRATION NUMBER: 30,092
REFERENCE DOCKET NUMBER: ABIC-001/01US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843 5070
TELEPHONE: (415) 857-0663
TELEFAX: 380816 COOLEYAR
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   , OTHER INFORMATION: AOA-Glu
US-08-114-877A-10
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                                                                                                                            12 OPLALEGSLOK 22
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US-09-633-269-10

Sequence 10, Application US/09633269

Sequence No. 666369

GENERAL INFORMATION:
PAPLICATION:
PAPLICANT: Keith, Rose

APPLICANT: Keith, Rose

APPLICANT: Cofford, Robin E

TITLE OF INVENTION: POLYOXIME COMPOSITIONS AND THEIR PREPARATION
FILE REFERENCE: CREN-001/03US

CURRENT FILING DATE: 2000-08-04

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: US/08/537,928

PRIOR PELING DATE: FARLIER FILING DATE: 1996-01-05

PRIOR PAPLICATION NUMBER: BARLIER APPLICATION NUMBER: PCT/IB94/00093

PRIOR PILING DATE: EARLIER FILING DATE: 1994-05-05

PRIOR APPLICATION NUMBER: BARLIER APPLICATION NUMBER: 08/105,904

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/105,904

PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/105,904

PRIOR PILING DATE: EARLIER FILING DATE: 1993-08-31

PRIOR PILING DATE: EARLIER FILING DATE: 1993-08-31
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JEGUREAL INCORMATION:
APPLICANT: Keith, Rose
APPLICANT: Keith, Rose
APPLICANT: Keith, Rose
APPLICANT: Keith, Rose
TITLE OF INVENTION: POLYOXIME COMPOSITIONS AND THEIR PREPARATION
TITLE OF INVENTION: POLYOXIME COMPOSITIONS AND THEIR PREPARATION
CURRENT APPLICATION NUMBER: US/08/537,928
CURRENT APPLICATION NUMBER: PCT/1B94/00093
EARLIER FILING DATE: 1994-05-05
EARLIER FILING DATE: 1993-08-31
EARLIER FILING DATE: 1993-08-31
EARLIER FILING DATE: 1993-08-31
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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100.0%; Score 53; DB 4;

Best Local Similarity 100.0%; Pred. No. 0.00037;

Matches 11; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: SITE
LOCATION: (1)
CTHER INFORMATION: Aminooxyacetyl-Glu
US-08-537-928-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1); OTHER INFORMATION: Aminooxyacetyl-Glu US-09-633-269-10
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0; Gaps

US-08-537-928-10 ; Sequence 10, Application US/08537928

RESULT 3

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Sequence 23, Appl
Sequence 24, Appl
Sequence 3, Appli
Sequence 3, Appli
Sequence 13, Appli
Sequence 13, Appli
Sequence 13, Appl
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                                                                                                         ; Search time 143.795 Seconds (without alignments) 24.802 Million cell updates/sec
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| cgn2 6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USO_NEW_PUB.pep:*
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| cgn2 6/ptodata/2/pubpaa/USO_NEW_PUB.pep:*
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| cgn2 6/ptodata/2/pubpaa/USOB_NEW_PUB.pep:*
| cgn2 6/ptodata/2/pubpaa/USOB_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-10-740-098-4

US-09-815-229-13

US-09-878-88-8

US-10-140-098-4

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US-10-028-410-8

US-10-044-326-2
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                                                                                                         October 28, 2004, 10:54:39;
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Maximum Match 100%
Listing first 45 summaries
                                                                        OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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53
1 QPLALEGSLQK 11
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Match Length
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Sequence 4, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 6, Appli
Sequence 1, Appli
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Sequence 2, Appli
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Sequence 2, Appli
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Suguence 23, Application US/10617568

Publication No. US20040197862A1

GENERAL INFORMATION:

APPLICANT: Dana-Farber Cancer Institute, Inc. et al.

TITLE OF INVENTION: GENERATION OF MHC CLASS II COMPOUNDS BY TITLE OF INVENTION: GENERATION OF MHC CLASS II COMPOUNDS BY TITLE OF INVENTION: PEPTIDE EXCHANGE

FILE REFERENCE: DRN. OF 1200-07-12

FRIOR FILING DATE: 2003-07-11

PRIOR APPLICATION NUMBER: 60/39584

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-12

PRIOR FILING DATE: 2002-07-22

NUMBER OF SEQ ID NOS: 36

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 23

LENGTH: 18
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S US-10-444-262-2

US-10-444-649-2

US-10-444-649-2

US-09-947-563-4

US-09-947-563-5

US-09-915-229-3

US-09-815-229-3

US-09-815-229-3

US-09-815-229-3

US-09-815-229-3

US-09-815-229-3

US-10-816-816-1

US-10-816-816-1

US-10-316-817-1

US-10-316-817-2

US-10-318-817-2

US-10-318-817-2

US-10-318-817-2

US-10-318-817-2

US-10-318-817-2

US-10-318-817-3

US-10-318-3

US-10-318-3
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  Query Match
Best Local Similarity 100.
Matches 11; Conservative
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ORGANISM: Homo sapiens
  RESULT 2
US-10-641-834-24
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Sequence Sequence

Sequence 1, Ap Sequence 4, P Sequence 2, P

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Subjection US/10740098

Publication No. US20040138101A1

GENERAL INFORMATION:
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US-09-947-563-3
                                        STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Escherichia coli
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                            CITY: Washington
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Best Local Similarity
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US-10-740-098-4
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; ORGANISM: Hc
US-10-740-098-4
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Sequence 3, Application US/09947563
Sequence No. US20020156234A1
GENERAL INFORMATION: Franz-Josef
APPLICANT: Rubroder, Franz-Josef
TITLE OF INVENTION: Improved process for obtaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Filaroff, Ellen H.
APPLICANT: Okumu, Franklin W.
TITLE OF INVENTION: USE OF INSULIN FOR THE TREATMENT OF CARTILAGENOUS DISORDERS
TITLE REFERENCE: P1766R1US
CURRENT APPLICATION NUMBER: US/09/815,229
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/192,103
PRIOR FILING DATE: 2000-03-24
NUMBER OF SEQ ID NOS: 17
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                                                          APPLICANT: Russell, Stephen James
APPLICANT: Russell, Stephen James
APPLICANT: Russell, Kah Whye
TITLE OF INVENTION: SYSTEM FOR MONITORING THE EXPRESSION OF
TITLE OF INVENTION: TRANSGENES
FILE REFERENCE: 07039-292002
CURRENT APPLICATION NUMBER: US/10/641,834
CURRENT APPLICATION NUMBER: 09/639,667
PRIOR APPLICATION NUMBER: 60/149,168
PRIOR FILING DATE: 1999-08-17
NUMBER OF SEQ ID NOS: 31
SOFFWARE: FRSESQ for Windows Version 4.0
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farrabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 100.0%; Score 53; DB 17; Length 33; 1 Similarity 100.0%; Pred. No. 0.0041; 11; Conservative 0; Mismatches n. Tadala
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: C-peptide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/09815229
Patent No. US20020058614A1
GENERAL INFORMATION:
US20040209830A1
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Best Local Similarity 100.
Matches 11; Conservative
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US-09-815-229-4
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Matches 11; Conserv
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LENGTH: 33
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Sequence:

Run on:

us-10-783-095-9.rge

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A48809 Sequence 1
A48810 Sequence 2
A61947 Sequence 2
A61947 Sequence 2
A81309 Novel vecto
102017 Sequence 6
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E00074 DNA sequence 1
114159 Sequence 12
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114161 Sequence 14
114161 Sequence 14
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A07328 Synthetic D
A07328 Synthetic D
A07328 Synthetic D
A11940 Nucleotide
112514 Sequence 41
112515 Sequence 42
113722 Sequence 28
A8275652 Sequence 28
A8275652 Sequence 28
BE006808 Method fo
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103224 Sequence 4
103602 Sequence 4
103602 Sequence 15
107905 Sequence 17
107905 Sequence 17
107906 Sequence 17
107907 Sequence 
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   I01821 Sequence 6
AR077833 Sequence
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Shin,H.-C., Chang,S.-G., Kim,D.-Y. and Kim,C.-S.
Proinsulin derivative and process for producing human insulin
Patent: US 562267-A 18 05-OCT-1999;
Location/Qualifiers
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Seguence 18 from patent US 5962267.
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A11939
A11939
A11936
I12514
I13722
AR275652
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BT006808
BT00778
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SYNINSGS
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AR134709
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Query Match:
DB:
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TITLE
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AR077834
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AX107018 Sequence
V01461 Synthetic g
AX179492 Sequence
                                                                                            October 28, 2004, 11:41:36; Search time 721.759 Seconds (without alignments) 720.721 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                   nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                    4526729 seqs, 23644849745 residues
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Maximum Match 100%
Listing first 45 summaries
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AX107018
XXHSIN
AX179492
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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Maximum DB seq length: 2000000000
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                                                                  OM protein
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No No Result

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shann, A., kerlero de Rosbo, N. and Sappler, G.P.
Synthetic human genes and polypeptides and their use in the stratuent of anterimmune diseases
Lreatuent of anterimmune diseases
Location/Qualifiers

rec | And Development CO. LTD. (LL)
Location/Qualifiers

rec | Anolary Synthetic construct"
| Mol type="unassigned DNA"
| Mol type="unassigned DNA"
| L. 207
| L. 207
| L. 207
| L. 207
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Sequence 87 from Patent WO0131037.
AX179492
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artificial sequences.
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TITLE
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AX179492
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                                                                ORIGIN
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V01461.1 G1:88303
3 artificial gene; gene synthesis.
Synthetic construct synthetic construct synthetic construct artificial sequences.
ISM synthetic construct synthesis of the human insulin gene. Part III. Chemical synthesis of 5'-phosphomonoester group containing deoxyribooligonucleotides by the modified phosphotriester method. Its application in the synthesis of seventeen fragments constituting human insulin C-chain synthesis of seventeen fragments constituting human insulin C-chain
                                                                                                                               PAT 30-APR-2001
                                                                                                                                                                                                                                                                     Habermann, P., Ertl, J., Meiwes, J. and Seipke, G.
C-peptide for the improved production of insulin and insulin
analogues
Patent: WO 0125278-A 1 12-APR-2001,
Aventis Pharma Deutschland GmbH (DE)
Location/Qualifiers
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                                                                                                                                 linear
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11
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Matches:
Conservative:
Mismatches:
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                                    1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
                                                    7 CAGCCGTTGGCGCTGGAAGGTTCCCTGCAGAAA 39
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Sequence 1 from Patent WO0125278.
AX107018
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      US-10-783-095-9 (1-11) x AR077834 (1-68)
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AX107018
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à Вb

Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

1 OPLALEGSLOK 11 US-10-783-095-9 53

Title: Perfect score:

Sequence:

protein

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Run on:

BLOSUM62

Scoring table:

100%

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100

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Adh21708 Human ins
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Aat17830 Human ins
Aat6905 Gene for
Aat6001 Human pro
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Aag7003 Perinsuli
Aag7003 Perinsuli
Aag7055 Synthetic
Aag7055 Synthetic
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Aag7055 Synthetic
Aag7055 Chelltied
Aar15230 Noci-Sell
Aag7025 Chellting
Aag7038 Oligonucl
Aag7019 Sequence
Aan6019 Sequence
Aan6019 Sequence
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Aan6019 Sequence
Aan6019 Sequence
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Aac7562 Human ins
Aac7562 Human ins
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chimeric fusion protein; immunodominant epitope; glutamate decarboxylase; daz, insulin; imsulin chain B; human T cell response; GADG5 peptide; Type I diabetes; insulin dependent diabetes mellitus; IDDM; Stiff Man syndrome; transplant; pancreatic cell; PCR primer; ss.
                                                                                                                                                                                                                                                                                                     Aat75652 Human ins
Aac55717 Mutant hu
Aaf58802 Human ins
Aas04761 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                             PCR primer used to produce chimeric genes of the invention.
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AAN70988
AAT37134
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ADF16306
ADH21708
ADI04119
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AAT17830
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AAQ383195
AAQ38319
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AAZS9208
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AAT75652
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AAF58802
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                                                                                                                                                                                                                                                                                                                                                                                         AAX86082 standard; DNA; 66
                                                                                                                                                                                                                                                                                                                                                                                                                           15-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALEXION PHARM INC.
MUELLER J P.
MATIS L A.
WO9932136-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-DEC-1998;
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Synthetic.
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AAX86082/c
Aax86082 PCR prime
Aaf61522 Human pro
Aat45977 Oligonucl
Aat45973 DNA encod
Aat45974 DNA encod
Aas04793 Synthetic
                                                        October 28, 2004, 11:40:21; Search time 143.398 Seconds (without alignments) 402.682 Million cell updates/sec
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                                                                                                                                                                                               8269772
      GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                        nucleic search, using frame_plus_p2n model
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AAX86082 AAF61522 AAT45977 AAT45973 AAT45974

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1000.0 1000.0 1000.0 1000.0

2222223

126450

DB

Length

Query

Score

. 02

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Result

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| Geneseq_12001as:*
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| Geneseq_12001as:*

Database :

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Chimeric fusion proteins comprising immunodominant epitopes of glutamate decarboxylase and insulin, used to treat patients that have or are predicted to be at risk of developing Type I diabetes.
                                                             Example; Page 62; 67pp; English
Wang Y;
Matis LA,
Mueller JP,
#X#X###X#X#X
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The specification describes chimeric fusion proteins comprising immunodominant epitopes of glutamate decarboxylase (GAD) and insulin. The chimunodominant epitopes of glutamate decarboxylase (GAD) and insulin. The chimunodominant epitopes of glutamate decarboxylase (GAD) and insulin. The consisting of at least one GAD65 peptide capable of eliciting a human T cell response, where the insulin chain B and GAD65 peptide are covalently linked and the chimuric fusion protein is capable of eliciting a human T cell response to insulin chain B and to each of the at least one GAD65 peptides. The chimuric fusion proteins are used to treat patients that are predicted to be at risk of developing Type I diabetes and those suffering from Type I diabetes mellitus (IDDM) and/or Stiff Man syndrome. This is also useful for determining the suitability of patients as recipients of transplants of the invention

Sequence 66 BP; 10 A; 27 C; 21 G; 8 T; 0 U; 0 Other;

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000
     Length:
Matches:
Conservative:
Mismatches:
Indels:
                                             Gaps:
     0.0131
53.00
100.00$
100.00$
                      Percent Similarity:
Best Local Similarity:
Alignment Scores:
                                      Query Match:
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US-10-783-095-9 (1-11) x AAX86082 (1-66)

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1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
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AAF61522 standard; DNA; 87 04-JUL-2001 AAF61522 RESULT 2 AAF61522

(first entry)

Human proinsulin C-peptide encoding DNA.

Insulin; proinsulin; C-peptide; human; B-chain; A-chain; diabetes; ds.

DE19947456-A1 Homo sapiens

02-OCT-1999;

99DE-01047456

99DE-01047456 02-OCT-1999; (AVET) AVENTIS PHARMA DEUT GMBH.

Seipke G;

Meiwes J,

Habermann P, Ertl J,

WPI; 2001-267042/28. P-PSDB; AAB70847 New synthetic derivatives of the C-peptide of proinsulin, useful in the

This invention describes novel synthetic derivatives (1) of the C-peptide of proinsulin. Such novel derivatives of human insulin or insulin analogs crepresented by (1) are of formula Rus-Bil-30. PRDP PYNA(1-21). Fus = optionally present fusion component of arbitrary sequence, B(1-30) = the coptionally present fusion component of arbitrary sequence, B(1-30) = the b-chain of human insulin, Y = amino acid chain having a basic amino acid cat the C-terminal, n = 2-50 (defining the chain length of Y), and A(1-21) = the A-chain of human insulin, the A- and/or B-chain(s) may be modified by amino acid exchanges, additions and/or deletions. (1) are considered acts for human insulin or its analogs, which are used in the corn of diabetes. A claimed method of preparing human insulin can form, enzymatically removing the RDVP-Yn part and compared in increased yields via (1). Specifically the expression yield can be increased around 20% compared with that obtained using plasmid compared in increased around 20% compared with that obtained using plasmid conformation and almost 5-fold compared with that obtained using plasmid concoded by plany90d. This sequence encodes the human proinsulin C-peptide which is described in the method of the invention preparation of human insulin or insulin analogs in high yield Sequence 87 BP; 10 A; 27 C; 37 G; 13 T; 0 U; 0 Other; Length: Matches: Conservative: Mismatches: CAGCCCTTGGCGCTGGAGGGTCCCTGCAGAAG 84 1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11 US-10-783-095-9 (1-11) x AAF61522 (1-87) Disclosure; Page 7; 12pp; German. 53.00 100.00% 100.00% Best Local Similarity: Percent Similarity: Alignment Scores: 52 Query Match: d

BP. AAT45977 standard; cDNA; 159

Oligonucleotide for 3' end of single chain insulin. 16-MAR-1997 (first entry)

Single chain insulin; diabetes mellitus; gene therapy; ss. 96EP-00303133 03-MAY-1996; 96-NON-1996 EP741188-A2 Synthetic

95US-00435503. 95US-00435762. & CO ELI (ELIL) LILLY 05-MAY-1995; 05-MAY-1995;

Miller AR; Long HB, Dimarchi RD, Hoffmann JA, WPI; 1996-487391/49 Chance RE,

Single chain insulin polypeptide(s) - used for treating diabetes. Example 7; Page 15; 22pp; English

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Sequence 12, Appl
Sequence 13, Appl
Sequence 41, Appl
Sequence 42, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 3, Appl
Sequence 1, Appl
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Sequence 12, P
Sequence 13, P
Sequence 3, Ag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 1
US-08-600-783-18
isequence 18, Application US/08600783
jsetent No. 596267
jsetent No. 5962267
jsetent Normanion is Applicant CHANG, Seung Gu
APPLICANT: KIM, Dae Young
jsetent KIM, Hang Cheol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: Seoul
CCUMTRY: Republic of Korea
ZIP: 135-110
ADDRESSEE: KIM, Dae Young
STREET: Sosa Jukong Apt. 108-202, Sosa Bon-dong,
STREET: Bucheon-shi
STATE: Kyungki-do
CCUMTRY: Republic of Korea
                                                                          US-08-030-731A-42
US-07-826-928A-28
US-07-696-551B-12
US-08-472-701-1
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CITY: Kwangmyung-shi
STATE: Kyungki-do
COUNTRY: Republic of Korea
ZIP: 423-030
ADDRESSEE: CHANG, Seung Gu
STREET: Hyundai Apt. 71-203, Apkujong-dong,
STREET: Kangnam-ku
                                                                                                                                                 PCT US95-08596-1
US-09-280-030-49
US-08-784-502-3
US-08-785-271-3
US-08-245-14-65
US-08-245-14-5
US-09-185-852-1
US-09-323-738-1
US-09-313-738-1
US-09-314-953-7
US-08-081-661-7
US-08-081-661-7
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US-09-75-508C-7
US-09-015-399-10
US-09-485-286-9
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US-09-485-286-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-537-696-11
US-09-537-696-12
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US-07-918-953-3
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STREET: Garden Heights Apt. 202-801, #100,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
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       422-230
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       CITY:
       Command line parameters:
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-MODEL=frame+ pin.model -DEV=xlp
-MODEL=frame+ pin.model -DEV=xlp
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Sequence 17, Appli
Sequence 10, Appli
Sequence 12, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 16, Appl
Sequence 16, Appli
Sequence 3, Appli
Sequence 2, Appli
                                                                                                                                 ; Search time 32.6024 Seconds (without alignments) 239.819 Million cell updates/sec
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4: /cgn2_6/ptodata/lina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/lina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/lina/PCTUS_COMB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                  nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-600-783-18
US-09-676-787-1.
US-08-673-312-10
US-07-918-953-12
US-07-918-953-14
US-08-081-661-12
US-08-081-661-12
US-08-081-661-14
US-08-081-661-16
US-07-715-183C-3
US-07-715-183C-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     October 28, 2004, 11:54:47
                                                                                                                                                                                                                                                                                 BLOSUM62
Xgapop 10.0, Xgapext
Ygapop 10.0, Ygapext
Fgapop 6.0, Fgapext
Delop 6.0, Delext
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Maximum DB seq length: 200000000
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53
1 QPLALEGSLOK 11
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Match Length
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Perfect score:
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No.
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GENERAL INFORMATION:
APPLICANT: SHIN, Hang Cheol
APPLICANT: CHANG, Seung Gu
APPLICANT: KIM, Dae Young
APPLICANT: KIM, Chong Suhl
TITLE OF INVENTION: Proinsulin Derivative and Process
TITLE OF INVENTION: for Producing Human Insulin
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: XIM, Chong Suhl
STREET: Garden Heights Apt. 202-801, #100,
STREET: Hwangkeum-dong, Scosung-ku
CITY: Taegu
CITY: Taegu
COUNTRY: Republic of Korea
ZIP: 706-040
COMPUTER READALE FORM:
MEDIUM TYPE: Floppy Disk, 3.5 inch, 1.44MB storage
COMPUTER: IBM PC/AT
    10000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: Republic of Korea
ZIP: 135-110
ADDRESSEE: KIM, Dae Young
STREET: Sosa Jukong Apt. 108-202, Sosa Bon-dong,
STREET: Sosa-ku
                 Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: CHANG, Seung Gu
STREET: Hyundai Apt. 71-203, Apkujong-dong,
STREET: Kangnam-ku
                                                                                                                                                                                                        52 CAGCCCTTGGCGCTGGAGGGGTCCCTGCAGAAG 84
                                                                                                                          US-10-783-095-9 (1-11) x US-09-676-787-1 (1-87)
                                                                Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SHIN, Hang Cheol
STREET: Ssangma-Hanshin Apt. 102-1206,
STREET: #245 Cholsan-dong
                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLACATE:
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-2751
FILING DATE: 15-FEB-1995
ATORNEY/AGENT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,783
                                                                                                                                                                                                                                                                                     Sequence 17, Application US/08600783
Patent No. 5962267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Bucheon-shi
STATE: Kyungki-do
COUNTRY: Republic of Korea
ZIP: 422-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kyungki-do
: Republic of Korea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (212) 953-7249
INFORMATION FOR SEQ ID NO: 17
  53.00
100.00%
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Kwangmyung-shi
STATE: Kyungki-do
COUNTRY: Republic of
                        Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seoul
                                                                                                                                                                                                                                                                        JS-08-600-783-17
                                                              Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: BRILL, Johann
APPLICANT: BRILL, Johann
APPLICANT: BRILL, Johann
APPLICANT: BRILL, Johannes
APPLICANT: MINES, Johannes
APPLICANT: SIPKE, Gerhard Bernard Gerhard
TITLE OF INVENTION: C PEPTIDE FOR IMPROVED PREPARATION OF INSULIN AND INSULIN ANALOGS
FILE REPERENCE: 38005-0110
CURRENT APPLICATION NUMBER: US/09/676,787
CURRENT APPLICATION NUMBER: US 199 47 456.7
PRIOR FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 13
SEQ-TUD NO 1
LENGTH: 87
TYRE: DNA
TYRE: DNA
CORRANSEM: Homo sapiens
US-09-676-787-1
                                                                                      ZLF: '.ve-va-v
COMPUTER READABLE FORM:
NEDIUM TYPE: Floppy Disk, 3.5 inch, 1.44MB storage
COMPUTER: IBM PC/AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-10-783-095-9 (1-11) x US-08-600-783-18 (1-68)
Hwangkeum-dong, Soosung-ku
                                                                                                                                                    OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,783
FILING DATE:
                                                                                                                                                                                                                                                      TLING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 95-2751
FILING DATE: 15-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAWE: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER:
TELEPHONE: (212) 278-1000
TELEPHONE: (212) 278-1000
TELEPHONE: (212) 953-7249
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09676787
Patent No. 6534288
GENERAL INFORMATION:
APPLICANT: HABERMANN, Paul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
             CITY: Taegu
STATE: Taegu
COUNTRY: Republic of Korea
ZIP: 706-040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.00%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alignment Scores:
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OM protein

Run on:

Sequence:

Searched:

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Sequence 43, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 1, Appli
Sequence 44, Appli
Sequence 44, Appli
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21, Appl
21, Appl
21, Appl
11, Appl
11, Appl
49, Appl
10, Appl
5, Appl
11, Appl
12, Appl
13, Appl
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17, Appl
18, Appl
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9, Appli
14, Appl
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| Sequence 1, Application US/10383285 |
| Publication No. US20030200566A1 |
| APPLICANT: HOWARD, JOHN |
| TITLE OF INVENTION: PLANTS |
| TITLE OF INVENTION OWNER: 00/3-05-21 |
| PRIOR PILLING DATE: 2003-05-21 |
| SEQ ID NOS: 2 |
| SEQ ID NO 1 |
| LENGTH: 258
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                                                                Sequence 1, Ag
Sequence 16, B
Sequence 17, B
Sequence 23, B
Sequence 21, B
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Sequence 43,
Sequence 43,
Sequence 43,
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Sequence 42
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Sequence
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0 US-09-807-742-16

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0 US-10-321-717-1

US-09-280-030-49

US-09-280-030-49

US-09-280-030-49

US-09-280-030-49

US-09-280-030-49

US-09-280-030-49

US-10-321-717-1

US-09-280-030-49

US-10-411-036-43

US-10-411-036-43

US-10-410-967-43

US-10-410-967-43

US-10-410-967-43

US-10-410-91-43

US-10-410-91-32

US-10-410-91-32

US-10-410-91-32

US-10-410-91-32

US-10-410-91-32

US-10-410-91-32

US-10-410-91-32

US-10-410-91-32

US-10-410-91-47

US-10-410-91-47

US-10-410-41-47

US-10-410-539-4
                       Length
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10512
10512
10880
10895
11255
11271
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CAGANISM: Homo sapiens
US-10-383-285-1
Query
Match
                                                                     RESULT 1
Result
No.
                                                                                                                                                                                                                                            Command line parameters:
-WODEL=frame+ p2n.model -DEV=xlp
-WODEL=frame+ p2n.model -DEV=xlp
-WODEL=frame+ p2n.model -DEV=xlp
-WODEL=frame+ p2n.model -DEV=xlp
-D=/CODE_1/USPTO spool p/US10783095/runat_26102004_185428_24911/app_query.fasta_1.796
-D3=/CODE_1/USPTO spool p/US10783095/runat_2610204_185428_24911/spendent -DOPEL=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -STRAT=1 -END=-1 -WATRIX=blosum62
-TRANS=humanq-0.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTPMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000000 -USBR=S10783095 @CGN 1 1.189 @runat_2610204_185428_24911
-NCPU6= .ICV=3 NO MAAP -LARGEQUERY NEG SCORES=0 -WAIT -DSPBLOCK=100
-LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRRADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
                                                                                                                                                                    ; Search time 127.494 Seconds (without alignments) 442.402 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications NA:*

1. /cgn2_6/ptodata/2/pubpna/PCT_PUBCOMB.seq:*
2. /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
3. /cgn2_6/ptodata/2/pubpna/PCT_NEW PUB.seq:*
4. /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
5. /cgn2_6/ptodata/2/pubpna/USO6_PUBCOMB.seq:*
6. /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
7. /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
8. /cgn2_6/ptodata/2/pubpna/USO8_NEW PUB.seq:*
9. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
10. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
11. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
13. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
14. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
15. /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
15. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
16. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
17. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
18. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
19. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
19. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
20. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
20. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
20. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
20. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
20. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
21. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
22. /cgn2_6/ptodata/2/pubpna/USOD_PUBCOWB.seq:*
                         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                        nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3413475 segs, 2563800928 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                       October 28, 2004, 13:47:02
                                                                                                                                                                                                                                                                                                                                                                                          Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                         US-10-783-095-9
53
1 QPLALEGSLOK 11
                                                                                                                                                                                                                                                                                                                    QPLALEGSLQK 11
                                                                                                                                                                                                                                                                                                                                                                  BLOSUM62
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                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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Jatabase :

us-10-783-095-9.rnpb

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APPLICANT: Cooper, Richard K.
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US-09-807-742-16
US-09-807-742-16
US-09-807-742-16
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US-09-807-742-16
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US-09-807-742-16
US-09-807-742-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-807-10-8
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TITLE OF INVENTION: PRODUCTION OF PHARMACEUTICAL PROTEINS IN TRANSGENIC
TITLE OF INVENTION: PAGDUCTION OF PHARMACEUTICAL PROTEINS IN TRANSGENIC
TITLE OF INVENTION: PAGDINGS
FILE REFERENCE: 1465-PCT-425.00
CURRENT APPLICATION NUMBER: US/09/807,742
PRIOR APPLICATION NUMBER: PCT/US01/06288
PRIOR APPLICATION NUMBER: PCT/US01/06288
PRIOR APPLICATION NUMBER: PCT/US01/06288
SOFTWARE: PAGDINGS: 19
SEQ ID NOS: 19
SEQ ID NO 17
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Description of Artificial Sequence: Chloroplast COTHER INFORMATION: modified proinsulin sequence
                                   Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
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                                                                                                                                                                                                                                                                                                                                                                   1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
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                                                                                                                                                                                                                                                                                           US-10-783-095-9 (1-11) x US-10-383-285-1 (1-258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 17, Application US/09807742; Publication No. US20030204864A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
                               0.0152
53.00
100.00%
100.00%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.0153
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100.00%
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ORGANISM: Homo sapiens
                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
DB:
Alignment Scores:
Pred. No.:
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Pred. No.:
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WESULT 46-149-23

Sequence 22, Application US/10746149

Publication No. US20040172667A1

Sequence 22, Application US/10746149

Publication No. US20040172667A1

SEQUENCE CONTROLLY COOPER. Richard K.

APPLICANT: Codd, Gary G.

APPLICANT: Cadd, Gary G.

APPLICANT: Cadd, Gary G.

TITLE OF INVENTION: Administration of Transposon-Based Vectors to Reproductive Organs

FILE REPERBENCE: 5169-0280 (51687-29423)

CURRENT FILING DATE: 2003-12-24

PRIOR APPLICATION NUMBER: US 60/441,491

PRIOR APPLICATION NUMBER: US 60/441,405

PRIOR FILING DATE: 2003-01-21

PRIOR FILING DATE: 2003-01-21

PRIOR PLING DATE: 2003-
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Matches:
Conservative:
Mismatches:
                                                                                                    Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                160 CAACCTTTAGCTTTAGAAGGTTCTTTACAAAAA 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    160 cagcccrrgcccrrgaagacccracagaag 192
                                                                                                                                                                                                                                                                                                                                                   1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
                                                                                                                                      Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GlnProLeuAlaLeuGluGlySerLeuGlnLys 11
                                                                                                                                                                                                                                                                            US-10-783-095-9 (1-11) x US-09-807-742-17 (1-260)
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Publication No. US20040197910A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: Synthetic US-10-746-149-23
                             0.0153
53.00
100.00%
100.00%
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100.00%
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Best Local Similarity:
Query Match:
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Best Local Similarity:
Alignment Scores:
Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

October 28, 2004, 10:16:44; Search time 8.87952 Seconds (without alignments) 119.194 Million cell updates/sec Run on:

US-10-783-095-9 53 1 QPLALEGSLQK 11 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 segs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	precursor	5				insulin precursor	ycf35 protein - Sy	glutamine-fructose	ical	integrase - Lactoc	prophage pi2 prote	integrase - phage	glutamine-fructose	glutamine-fructose	glutamine-fructose	glutamine-fructose	hypothetical prote	proteinase IV [imp	type II restrictio	ΙI	2.	Hsp70 cofactor (im	netic	-6	ca a	ical	mine-f	amine-	glutamine-fructose
ID	IPHU	B42179	JQ0178	A42179	IPDG	IPGP	877068	PC4141	T25703	T13262	H86750	A47085	H71809	D64711	C81281	C97575	AC2796	AF2379	F95141	D98009	INRB	C87221	T40386 .	α	9028	901	7032	929	0104
DB		7	~	7	Н	Н,	~	N	N	N	N	N	(7)	N	~	~	7	8	~	~	Н	~	~	7	N	N	7	N	Н
Length	110	110	110	110	110	110	128	156	210	374	374	374	597	597	598	608	608	609	08	1084	٦	œ	വ	4	ω	591	σ	0	0
	. 0		0	00	94.3	77.4	77.4	61.9		67.9	67.9	•	۲.	67.9	•	67.9		67.9	ů.	è.	4.	4.	•		٠	64.2		64.2	64.2
Score		53			20	41	41	36	36	36	36	36	36	36	36	36	36		35		34	34	34	34		34	34	34	34
Result No.	1	7	m	4	Ω.	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

NodM Glutamine ami	glutamine-fructose	glutamine-fructose	glutamine-fructose	glutamine-fructose	glutamine-fructose	glutamine-fructose	hypothetical prote	hypothetical prote	glutamine-fructose	glutamine-fructose	glutamine-fructose	glutamine-fructose	glutamine-fructose	Down syndrome cell	hypothetical prote
_															
B95322	XNECGM	. AB0955	B81528	F86611	E72012	A82844	H86058	G91212	T45493	B81246	H82022	AD3595	S74575	108851	877257
7	-1	7	2	7	7	7	7	~	7	7	7	~	C)	2	N
609	609	609	609	609	609	609	609	609	611	612	612	612	631	1896	1978
64.2	2.	1.2	. 2	2.	2.	2.	7.	7.5	7.	.2	7.5	.2	2	64.2	. 2
64	64	64	64	64	9	9	64	9	9	9	9	9	9	9	9
34	34	34	34	34	34	34	34	34	34	34	34	34	34	34	34
3.0	31	32	33	34	33	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1		
IPHU insulin precursor [validated] - huma N;Alternate names: preproinsulin C:Species: Homo saciens (man)	- human in	
C,Date: 23-Oct-1981 #sequence revisi C,Accession: A93222; A94253; A93216; R;Bell, G.I.; Pictet, R.L.; Rutter,	C.Date: 23-Oct.1981 #sequence revision 23-Oct.1981 #text_change 09-Jul-2004 C.Accession: A93222; A94253; A93216; A94251; A93144; A92075; A91186; I58114; A01579 R.Pell, G.I.; Pictet, R.L.; Rutter, W.J.; Cordell, B.; Tischer, B.; Goodman, H.M.	1579; S58 4.
Nature 284, 28-32, 1590 A;Title: Sequence of the human insulin gene. A;Reference number: A93222; MUID:80120725; PMID:6243748	insulin gene. ID:80120725; PMID:6243748	
A, Accession: A93222 A, Molecule type: DNA		
A; Restauces: 1-110 cBELJ: A; Cross-references: UNIPROT:P01308; GB:J00265; NID:9186429; R;Ullrich, A:; Dull, T.J.; Gray, A.; Brosius, J.; Sures, I.	PIDN:AAA59172.1;	PID:9386828
Science 209, 612-615, 1980 A;Title: Genetic variation in the human insulin gene.	the human insulin gene.	
A;Reference number: A94253; MUID:802 A;Accession: A94253	ID:80236313; PMID:6248962	
A;Molecule type: DNA A;Residues: 1-110 <ull></ull>		
A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; R:Bell. G.I.: Swain, W.F.: Pictet, R.: Cordell, B.: Goodman,	NID:g186429; PIDN:AAA59172.1; PID:g386828 tet, R.; Cordell, B.; Goodman, H.M.; Rutter, W.J.	-
Nature 282, 525-527, 1979	minima namind specification of the second	
A;Title: Nucleotide sequence of a CD A;Reference number: A93216; MUID:800	A;Iltle: Nucleotide sequence or a cunA cione encoding numan preproznavin. A,Reference number: A93216; MUID:80054779; PMID:503234	
A; Accession: A93216		-
A;Residues: 1-110 <bel2></bel2>		
A; Cross-references: GB:J00265; NID:g186429;	NID:9186429; PIDN:AAA59172.1; PID:9386828	
K;sures, 1.; Goeddel, D.V.; Gray, A.; Ullica, Science 208, 57-59, 1980	dy, A.; Ullich, A.	
A; Title: Nucleotide sequence of huma	sequence of human preproinsulin complementary DNA.	
A; Reference number: A94251; MOID: 8014/41/; FMID: 892/640 A;Accession: A94251	ID:8014/41/; FMID:092/040	
A; Molecule type: mRNA		٠
A;Cross-references: GB:J00265; NID:9	A;Kesiddes: 1-110 <50K? A;Cross-references: GB:J00265; NID:g186429; PIDN:AAA59172.1; PID:g386828	
R; Nicol, D.S.H.W.; Smith, L.F.		
gge	of human insulin.	
A;Reference number: A93144		
A; Molecule type: protein		
R;Oyer, P.E.; Cho, S.; Peterson, J.D.; Steiner,	n, J.D.; Steiner, D.F.	
J. Biol. Chem. 246, 1375-1386, 1971	7	ימפת תפשוות
A,Title: Studies on human proinsulin. Isolation and ami A,Reference number: A92075; MUID:71116410; PMID:5101771	ווס שכות אפלתפווכה סד	naman pan
A, Accession: A92075		
A)MOLECUIE LYDE: PLOCELLI		

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A,Cross-references: UNIPROT:P30407; EMBL:X61092; NID:g22808; PIDN:CAA43405.1; PID:g22809
A;Note: sequence extracted from NCBI backbone (NCBIN:95185, NCBIP:95194)
B;Peterson, J.D.; Nehrlich, S.; Oyer, P.E.; Steiner, D.F.
J. Biol. Chem. 247, 4865-4871, 1972
A;Title: Determination of the amino acid sequence of the monkey, sheep, and dog proinsuli A;Reference number: A92111; MUID:72258016; PMID:4626369
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C;Species: Pan troglodytes (chimpanzee)
C;Date: 0.4 Mar.1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C;Accession: A42179; S22058
R;Seino, S.; Bell, G.I.; Li, W.H.
R;Seino, S.; Bell, G.I.; Li, W.H.
A)Cl. Biol. Bvol. 9, 193-203, 1992
A;Title: Sequences of primate insulin genes support the hypothesis of a slower rate of mc. A;Reference number: A42179; MUID:92219953; PMID:1560757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R,Wetekam, W.; Groneberg, J.; Leineweber, M.; Wengenmayer, F.; Winnacker, E.L.
6ene 19, 179-183, 1982
A;Title: The nucleotide sequence of CDNA coding for preproinsulin from the primate Macaca
A;Reference number: JQ0178; MUID:83080474; PMID:6184262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       insulin precursor - crab-eating macaque
C;Species: Macaca fascicularis (crab-eating macaque)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JQ0178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 110;
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                                                                                                                                                                                                                                                                                                                                                                                                                           C)Superfamily: insulin
C)Superfamily: insulin
C;Rewords: hormone, pancreas
F):1-24/Domain: signal sequence #status predicted <SIG>
F):25-54/Domain: insulin chain B #status predicted <BCH>
F):25-54/Domain: connecting peptide #status predicted <MAT>
F):57-97/Domain: connecting peptide #status experimental <F):90-110/Domain: insulin chain A #status predicted <ACH+
F):31-96,43-109,95-100/Disulfide bonds: #status predicted
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100.0%; Pred. No. 0.0011;
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100.0%; Pred. No. 0.0011;
live 0; Mismatches 0;
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Best Local Similarity luv...
Best Local 11; Conservative
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Best Local Similarity 100.
Matches 11; Conservative
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                                                                                                                                                                                                                                                                                          A;Molecule type: protein
A;Residues: 57-87 <PET>
   1-110 <SEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Molecule type: mRNA; Residues: 1-110 <WET>
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                                                                                                                                                                                                                                                       M.; Bell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A, Residues: 1-59,63-110 cRES>
A, Cross-references: GB:L15440; NID:g307071; PIDN:AAA59179.1; PID:g307072
A; Cross-references: GB:L15440; NID:g307071; PIDN:AAA59179.1; PID:g307072
R; Sieber., P.; Kamber, B.; Hartmann, A.; Joehl, A.; Riniker, B.; Rittel, W.
Helv. Chim. Acta 57, 2617-2621, 1974
A; Title: Totalsynthese von Humaninsulin unter gezielter Bildung der Disulfidbindungen.
A; Reference number: A91636; MUD:75077277; PMID:4443293
A; Contents: annotation; synthesis
A; Note: disulfide-bonded human insulin was synthesized; the synthetic hormone was idential apsirotle in German with English abstract.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoppe-Seyler's Z. Physiol. Chem. 354, 659-672, 1973
A;Title: The synthesis of C-peptide of human proinsulin.
A;Reference number: A91658; MUID:75040007; PMID:4803504
A;Contents: annotation; synthesis of residues 57-87
B;Geiger, R.; Jaeger, G.; Koenig, W.
Chem. Ber. 106, 2347-2352, 1973
A;Title: Synthesis of the complete sequence of human proinsulin C-peptide and its [Glu-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A/Reference number: A90914
A/Contents: annotation; synthesis of residues 57-87
R/Kaufmann, J.E.; Irminger, J.C.; Halban, P.A.
Biochem. J. 310, 869-874, 1995
A/Title: Sequence requirements for proinsulin processing at the B-chain/C-peptide junctiA/Reference number: S58661; MUID: 96013185; PMID: 7575420
A/Contents: annotation; site-directed mutagenesis study of proteolytic processing
                                                                                                                                                                                                  A;Residues: 57-87 cxOA>
A;Residues: 57-87 cxOA>
R;Lucassen, A.M.; Julier, C.; Beressi, J.P.; Boitard, C.; Froguel, P.; Lathrop, M.; Bell Nature Genet. 4, 305-310, 1993
A;Title: Susceptibility to insulin dependent diabetes mellitus maps to a 4.1 kb segment A;Reference number: I58114; MUID:93364428; PMID:8358440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         insulin precursor - green monkey
Cispecies: Cercopithecus acthiops (green monkey, grivet)
Cispecies: Ocropathecus acthiops (green monkey, grivet)
Cipate: 04-Mar.1993 #sequence revision 18-Nov-1994 #text_change 09-Jul-2004
Cipacession: B42179; A05222; 516494; S22056
Riseino, S.; Bell, G.I.; Li, W.H.
Mol. Biol. Evol. 9, 193-203, 1992
A/Title: Sequences of primate insulin genes support the hypothesis of a slower rate of A/Reference number: A42179; MUID:92219953; PMID:1560757
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R:Ko, A.; Smyth, D.G.; Markussen, J.; Sundby, F.
Bur. J. Blochem. 20, 190-199; 197.
A;Title: Amino acid sequence of the C-peptide of human proinsulin.
A;Reference number: A91186; MUID:71257722; PMID:5560404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F,25-54/Domain: insulin chain B stetus experimental cBCH>
F,25-54/Domain: insulin chain B status experimental cMAT>
F;57-9/TDomain: connecting C peptide #status experimental cCPEP>
F;57-9/TDomain: insulin chain A #status experimental cCPEP>
F;31-96,43-109,95-100/Disulfide bonds: #status experimental
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1-24/Domain: signal sequence #status predicted <SIG>
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A;Map position: 11p15.5-11p15.5
A;Introns: 63/1
C;Superfamily: insulin
C;Superfamily: insulin
F;1-24/Domain: signal sequence #status predi
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                                                                                                                                                                               A; Molecule type: protein
                                                                                                                                         Accession: A91186
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BO267254 118 bp mRNA linear EST 15-JUL-2003 ikOlb07.yl Human insulinoma Homo sapiens cDNA clone IMAGE:5779548 comilar to SW:INS_HUMAN P01308 INSULIN PRECURSOR. [1] ;, mRNA
        CA948611 1929207.x
BMS510922 1145511.x
BMS57672 1169101.x
BMS7747 1169101.x
BMS7747 1169101.x
BMS7747 1169101.x
BMS7747 1169101.x
BMS7777 1169101.x
BU7770546 11606101.x
BU7770545 1169101.x
BMS5510 1162602.x
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in19q07.x
im19q07.x
im35e06.y
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in56a07.y
ih16h03.x
ik34e02.x
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
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ik12a12.y
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ih24b05.x
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io40b12.y
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 118)

Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,

Emishkai,I., Scearce,M., Brestelli,J., Gradwohl,G., Clifton,S.,

Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,

Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,

Williams,T., Jackson,Y. and Bowers,Y.

Endocrine Pancreas Consortium

Unpublished (2000)
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Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SR- by Dr. H. Incue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
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BU71888
BU718188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 617-495-1812
Fax: 617-495-8557
 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seguence
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  RESULT 1
BQ267254/c
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-MODEL=frame+ Par.model -DEV=xlp
-MODEL=frame+ Par.model -DEV=xlp
-MODEL=frame+ Par.model -DEV=xlp
-CgnZ : 1/USFTO spool p/USIO783095/runat_26102004_185426_24817/app_query.fasta_1.796
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-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -ALIGN=15 -MODE=LOCAL
-OUTHWHEACO -THR SCORE=pct -THR MAX=100 -THR MINS 0 -ALIGN=15 -MODE=LOCAL
-OUTHWHEACO -NORM-ext -HEAPSIZE=500 -MINIEN=0 -NAXIEN=200000000
-USER=USIO783095_@CGN 1 19525_@runat_2610204_185426_24817 -NCFU=6 -ICFU=3
-NO_MMAP -LARREQUERY -NGG_SCORES=0 -MAIT -DSPBEICCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBLOR=6 -DBLEXT=7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BQ267254 1K01b07.7
BQ272508 1K01b07.x
BU073408 1m35e06.x
B1466830 1c59a08.x
B1466930 1c60g10.x
BU074185 1m85a02.x
BM511718 1194108.x
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                                                                           ; Search time 1251.08 Seconds (without alignments) 320.392 Million cell updates/sec
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Compugen Ltd.
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              GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
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Listing first 45 summaries
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BQ272508
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BI466930
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BU073285
                                                                             October 28, 2004, 11:54:21
                                                                                                                                                                             Xgapop 10.0 , Xgapext
Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
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AUTHORS
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                                                                                                                                                                                     /dine="INAGE:5779548"
/clone="INAGE:5779548"
/tissue_type="insulinoma"
/tlab.nst="BHIOB (phage-resistant)"
/lab.nst="BHIOB (phage-resistant)"
/clone_lib="Human insulinoma"
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Xhol; Site_2: BcoRi; Constructed with lambda ZAPII system
/knot; Site_2: BcoRi; Constructed with lambda ZAPII system
(Stratagne) by Dr. H. Inoue following the Washington
University protocol
(http://genome.wustl.edu/est/lambda_protocol:shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Mashington University School of Medicine, Box
8127, 660 S Bullid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BQ272508 118 bp mRNA linear EST 15-JUL-2003 ik01b07.x1 Human insulinoma Homo sapiens cDNA clone IMAGE:5779548 3' similar to SW:INS_HUMAN P01308 INSULIN PRECURSOR. [1] ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (2007)
Unpublished (2007)
Other ESTS: ikolbb7,y1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 118)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (Marses 1 C.) 110), Kenty, G., Permutt, A., Lee, C., Kaeetner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hiller, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCan, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y.
  (hinoue@im.wustl.edu)
                     Possible reversed clone: similarity on wrong strand
Seg primer: -40RP from Gibco.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
Mismatches:
Indels:
clone please contact: Dr. Hiroshi Inoue
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Email: dmelton@biohp.harvard.edu
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KEYWORDS
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/tissue_type="insulinoma"
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Xhoī; Site_2: EccRI; Constructed with lambda ZAPII system
(Stratagene) by Dr. J. Ferrer, in vivo mass-excised to
pBluescript SK- by Dr. H. noue following the Washington
University protocol
(http://genome-wustl.edu/est/lambda_protocol:shtml).
Please contact Hiroshi Inoue, MD/PhD for further
information on this library (Metabolism Division, Permutt
Laboratory, Washington University School of Medicine, Box
8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this
is a Washington University Pancreas EST project library."
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Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Scearce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marran, M., Pape, D., Wylie, T., Mortin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Williams, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and Bowers, Y. Cole, R., Tsagareishvili, R., Mnpublished (2000)
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Fax: 617-495-8557
Email: dmelton@blobp.harvard.edu
Library was constructed by Dr. J. Ferrer In vivo mass-excised to
pBluescript SK. by Dr. H. Inoue DNA sequencing by: Washington
University Genome Sequencing Center For information on obtaining
clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
   Inoue (hinoue@im.wustl.edu)
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Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave,
MA 02138
clone please contact: Dr. Hiroshi Inoue (hinoue@im.w
Possible reversed clone: similarity on wrong strand
Seq primer: -40UP from Gibco.
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P01329 cavia porce
Q91329 cavia porce
Q9133 spermophilu
Q55981 synchocyst
Q72cd0 desulfovibr
A8895831 desulfovi
Q88ab3 pseudomonas
Q96c24 homo sapien
Q8bi6 mus musculu
Q8tf50 homo sapien
Q9bef8 canis famil
Bac75929 canis fam
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P30407 cercopithec
P01308 homo sapien
P30406 macaca fasc
P30410 pan troglod
Q8hx2 pongo pygma
Q6yx3 gorilla gor
Aap35454 homo sapi
Aan06935 gorilla g
P01321 canis famil
P01321 cavia porce
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lactococcus
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Q8hz81 gorilla gor
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                                                       , Search time 38.9639 Seconds (without alignments) 162.436 Million cell updates/sec
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Q8wnw6 f
Q56206 s
P91262 c
Q7v7s5 F
Q38088 b
Q38313 b
                                                                                                                                                                                    1825181
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                 1825181 segs, 575374646 residues
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GHRL CANFA
BAC75929
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Q8WNW6
GLMS SPHYA
P91262
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Maximum Match 100%
Listing first 45 summaries
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INS CANFA
INS CAVPO
INS SPETR
255981
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                                      - protein search, using sw model
                                                         October 28, 2004, 06:48:48
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AAS95831
Q88AB3
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AAP35454
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8BI66
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038088
                                                                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
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1: uniprot_sprot:*
2: uniprot_trembl:*
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Maximum DB seq length: 2000000000
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Q38608 lactococcus Q9b016 bacteriopha Q9cgt4 lactococcus	Q7mau3 wolinella s Q9zj94 h glucosami O26060 h glucosami		P94323 bradyrhizob Q6sey6 uncultured Q726f2 desulfovibr Aar38436 unculture
Q38608 Q9B016 Q9CGT4	O7MAU3 GLMS_HELPJ GLMS_HELPY	GLMS_CAMUE Q7XSJ2 GLMS_AGRT5 GLMS_BRAJA	NODM BRAJA Q6SE¥6 Q726F2 AAR38436
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RANGE RELEASE

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100.0%; Score 53; DB 1; Length 110; 100.0%; Pred. No. 0.011; ive 0; Mismatches 0; Indels
       PROSITE; PS00262; INSULIN; 1.
Direct protein sequencing; Glucose metabolism; Hormone;
Insulin family; Signal.
                                                                                                                                                                                 12019 MW; 95A1F54BE7B247F9 CRC64;
                                                                                             C peptide.
Insulin A chain.
Interchain.
                                                                              Insulin B chain.
                                                                                                                                                  Interchain.
                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                               110 AA;
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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P01308;
21-JUL-1986
                                                                                                                            DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=92219933; PubMed=1560757;
Seino S., Bell G.I., Li W.;
"Sequences of primate insulin genes support the hypothesis of a slower rate of molecular evolution in humans and apes than in monkeys.";
Mol. Biol. Evol. 9:193-203(1992).
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   procedure.";
J. Biol. Chem. 247:4866-4871(1972).
-!- FUNCTION: Insulin decreases blood glucose concentration. It increases cell permeability to monosaccharides, amino acids and fatty acids. It accelerates glycolysis, the pentose phosphate cycle, and glycogen synthesis in liver.
-!- SUBUNIT: Heterodimer of a B chain and an A chain linked by two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peterson J.D., Nehrlich S., Oyer P.E., Steiner D.F., sheep, and "Determination of the amino acid sequence of the monkey, sheep, and dog proinsulin C-peptides by a semi-micro Edman degradation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecus aethiops (Green monkey) (Grivet).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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                                                                                                                                                                                          100.0%; Score 53; DB 2; Length 65; 100.0%; Pred. No. 0.006; tive 0; Mismatches 0; Indels
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65 65
65 AA; 6920 MW; B772017FD8BCABEA CRC64;
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-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the insulin family.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0005179; F:hormone activity; IEA.
GO; GO:0005179; F:physiological process; IEA.
InterPro; IPR004825; Ins/IGF/relax.
Pfam; PF00049; Insulin; 1.
Insulin family.
                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 25, Created)
(Rel. 25, Last sequence update)
(Rel. 44, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL, X61092; CAA43405.1; -. PIR; B42179; B42179; B42179; B42179; B42179; B42179; IA10.
INCEPPC: IPRO04825; INS/IGF/relax. PERN; PF00049; INSULINB.
PRINTS; PRO0277; INSULINB.
SMART; SMO00709; ILGF; 1.
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NCBI_TaxID=9534;
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SEQUENCE OF 57-87.
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P30407; P01309;
01-APR-1993 (Rel
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"Nucleotide sequence of a cDNA clone encoding human preproinsulin:"; Nature 282:525-527(1979).
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MEDLINE=93364428; PubMed=8358440;
Lucassen A.M., Bell J.I., Julier C., Lathrop M.;
"Susceptibility to insulin dependent diabetes mellitus maps to a 4.1
"Susceptibility to insulin dependent diabetes mellitus maps to a 4.1
"Kb segment of DNA spanning the insulin gene and associated VNTR.";
Nat. Genet. 4:305-310(1993).
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PABLINE=2388251, PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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MEDLINE=80147417; PubMed=6927840;
Surse I., Gededel D.V., Gray A., Ullrich A.;
"Nucleotide sequence of human preproinsulin complementary DNA.";
Science 208:57-59(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-80054779; PubMed-503234;
Bell G.I., Swain W.F., Pictet R.L., Cordell B., Goodman H.M.,
Rutter W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=80120725; Pubmed=6243748;
Bell G.I., Pictet R.L., Rutter W.J., Cordell B., Tischer
Goodman H.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDINE-80236313; PubMed=6248962;
Ullrich A., Dull T.J., Gray A., Brosius J., Sure
"Genetic variation in the human insulin gene.";
                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-OCT-2004 (Rel. 45, Last annotation update)
North Tracursor.
110 AA
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AAY33360 standard; protein; 294 AA.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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SUMMARIES

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	QI	AAY33360	AAY49854	AAW80486	AAY49329	AAY59351	AAY33361	AAY49855	AAW80487	AAY49330	ABU04788	ABU04790	ABU04792	ABU04791	ABU04783	ABU04785	ABU04795	AAR45779	ABU04786	ADE56165	ADD45276	ABB06112	AAR49039	ABU04787	AD060054	AAY06606
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ALIGNMENTS

CCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCCC	Human islet cell antigen clone ICA-512 protein fragment. Human islet cell antigen, ICA; human; pancreas; antibody; IDDM; immunoass; insulin-dependent type I diabetes mellitus; diagnosis; immunosiobul T-cell; B-cell; islet cell destruction; immunoreactivity; disease; immune therapy; stimulating antigen; screening. Homo sapiens. US595345-A. 21-SEP-1999. 06-JUN-1995; 95US-00468576. 17-FEB-1989; 89US-00312543. 04-DEC-1989; 91US-00312543. 04-DEC-1989; 91US-00131281. 08-JUN-1991; 91US-00131281. 08-JUN-1991; 91US-0013181. 08-JUN-1994; 94US-00239276. (FARE) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC. Rabin DU; WPI: 1999-560494/47. N-FSDB; AAZ09922. Isolated DNA encoding antigens reactive with serum from diabetics uto develop products for the diagnosis and monitoring of insulin-dep diabetes mellitus. Example; Col 85-87; 63pp; English. This invention describes novel isolated and purified DNAs encoding pancreatic islet cell antigens reactive with islet cell antibodies in serum from in sera of patence with insulin-dependent type I diabetes mellitus; in sera of patence with insulin-dependent type I diabetes mellitus; in sera of patence with insulin-dependent type I diabetes mellitus; in sera of patence with insulin-dependent type I diabetes mellitus; in sera of patence with insulin-dependent type I diabetes mellitus; (IDM). The polybestides of the invention are useful as immunoassay (IDM).	reagents diabetes
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AAY49849), ATCC 40551 (AAZ32336, encoding AAY49850), ATCC 40552 (AAZ33237, encoding AAY49852)
ATCC 40703 (AAZ32338, encoding AAY49853), ATCC 40705 (AAZ32340), ATCC 40706 (AAZ32344, encoding AAY49854) and ATCC 75030 (AAZ32342, encoding AAY49855). ICA proteins and their peptide fragments can be used in the diagnosis of IDDM and in detecting or blocking human immunoglobulin, Tells or B-cells involved in IDDM

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Gaps

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100.0%; Score 24; DB 2; Length 294; 100.0%; Pred. No. 4e-16; ive 0; Mismatches 0; Indels

110 KLKVESSPSRSDYINASPIIEHDP 133

1 KLKVESSPSRSDYINASPIIEHDP 24

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Matches

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Local Similarity

Query Match

Sequence 294 AA;

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antibody binding site on islet cell antibodies (ICAs) also confers
utility in the binding or blocking of human immunoglobulin, T-cells, or B
-cells involved in IDBM. The products can also be used to study the
biological mechanisms involved in islet cell destruction and the
appearance of ICA. The immunoreactivity profile with different antigens
can provide diagnostically significant information concerning the nature
of the disease, e.g. subtypes, the state of the disease, the proximity to
onset of the disease, and the efficacy of therapy, e.g. immune therapy.
The antigens can serve as stimulating antigens for T-cell culture,
permitting significantly improved T-cell cloning, identification, and
growth. The availability of large quantities of pure antigen enables the
development of highly sensitive and specific immunoassays which can be
to used to screen the general population of presymptomatic IDDM or a
predisposition to develop IDDM. This sequence represents the human islet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, pancreatic islet cell antigen, ICA clone, IDDM; diabetes,
insulin dependent type I diabetes mellitus, diagnosis, detection,
immunoglobulin, T-cell, B-cell, antibody binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                insulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen. The proteins are used for the diagnosis and treatment of insulin dependent (Type I) diabetes mellitus (IDDM). They are recognised by autoantibodies of the disease as IDDM is now thought to be an autoimmune disease. They were identified from probing of IDDM serum with human cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents a pancreatic islet cell antibody (ICA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                       Pancreatic islet cell antibody antigen; ICA antigen; diagnosis;
treatment; insulin dependent diabetes mellitus; IDDM; autoantibody;
autoimmune disease; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide antigens from pancreatic islet cells - useful for the detection and treatment of insulin dependent diabetes mellitus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 24; DB 2; Length 294; 100.0%; Pred. No. 4e-16; ive 0; Mismatches 0; Indels
                                                                                                            Islet cell antibody antigen encoded by clone ICA-512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      libraries expressing protein fragments
                          AAW80486 standard; protein; 294 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Col 51-54; 47pp; English.
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89US-00441703.
91US-00715181.
92US-00872646.
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Best Local Similarity 100.
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-034118/03.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAV63560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 294 AA;
                                                                                01-FEB-1999
                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                               05-MAY-1994;
                                                                                                                                                                                                                                                                                                          17-FEB-1989;
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08-JUN-1992
                                                      AAW80486;
                                                                                                                                                                                                                                                                                                                                                                                                         Rabin DU;
              AAW80486
RESULT
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1 KLKVESSPSRSDYINASPIIEHDP 24

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The present sequence represents a human pancreatic islet cell antigen (ICA) that binds with antibodies found in the sera of patients afflicted with insulin-dependent (Type 1) diabetes mellitus (IDDM). ICAS from the present invention are encoded by the DNA insert of a recombinant cloning vehicle selected from ATCC 40550 (AAZ32333, encoding AAY49847), ATCC 40553 (AAZ32334, encoding AAY49847), ATCC

New pancreatic islet cell antigens, useful in the diagnosis of insulindependent (Type 1) diabetes mellitus.

Claim 1; Col 83-86; 61pp; English.

CORP FORMERLY MOLECULAR DIAGNOSTIC.

(FARB) BAYER

Rabin DU;

WPI; 1999-633370/54.

N-PSDB; AAZ32341.

89US-00441703. 91US-00715181. 92US-00872646. 89US-00312543.

17-FEB-1989;

94US-00239276

08-JUN-1992; 05-MAY-1994; 14-JUN-1991;

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US-08-468-576B-18
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                                                                                                  October 28, 2004, 11:13:25 ; Search time 19.0843 Seconds (without alignments) 83.400 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
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US-08-468-5778-18
US-08-468-5778-19
US-08-468-5778-19
US-08-514-213A-2
US-09-15-298-28-41
US-09-552-8028-41
US-09-552-8028-41
US-09-552-8028-39
US-09-811-481-4
US-08-811-481-2
US-08-811-481-2
US-09-876-527-7
US-08-811-481-2
US-08-811-481-2
US-08-814-181-2
US-08-814-181-2
US-08-814-181-2
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                                                                                                                                                                                                                                                                                                  478139 segs, 66318000 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Listing first 45 summaries
                                                                   - protein search, using sw model
                                                                                                                                                                       US-10-783-095-12
24
1 KLKVESSPSRSDYINASPIIEHDP
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Gapop 60.0 , Gapext 60.0
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Maximum DB seq length: 2000000000
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818
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Perfect score:
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                                                                     OM protein
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Sequence 4, Application US/08884569A

Sequence 4, Application US/08884569A

Patent No. 639926

GENERAL INFORMATION:
HIPPORMATION:
PAPPLICANT: CHIANG, MING-KO

APPLICANT: FLANAGAN, JOHN G.

TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO

TITLE OF INVENTION NUMBER: US/08/884,569A

CURRENT APPLICATION NUMBER: 05/021,040

PRIOR FILING DATE: 1996-07-02

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 4

LENGTH: 246

TYPE: PRI

CURRENT STANISM: Mus Sp.

US-08-884-569A-4
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Patent No. 595345
GENERAL INPORMATION:
APPLICANT:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe CITY:
TITLE OF INVENTION:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe CITY:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe CONDUTER:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe COMPUTER:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe COMPUTER: Apple Macintosh
ADDRESSEE: Apple Macintosh
                                                                             US-08-015-985-6
US-09-280-597-6
US-09-144-925-26
US-09-144-925-24
US-08-144-925-24
US-08-144-925-24
US-08-144-925-10
US-08-685-992-10
US-08-685-992-10
US-08-685-992-14
US-08-144-925-14
US-08-144-925-14
US-08-144-925-16
US-08-144-925-16
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110 KLKVESSPSRSDYINASPIIEHDP 133
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FILING DATE: 04-DEC-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-PEB-1989
FILING DATE: 08-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity 100.0
Matches 24; Conservative
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US-08-468-577B-18
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Sequence 18, Application US/08468579B
Sequence 18, Application US/08468579B
Setent No. 5981700
GENERAL INFORMATION:
ADDELICANT: Rabin, Daniel
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10594-514
ZIP: 10594-514
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
                                CUREALI AFFLICATION DATA:
CLASSIFICATION NUMBER: US/08/468,576B
FILING DATE: O6-JUN-1995
CLASSIFICATION NUMBER: US 08/239,276
FILING DATE: O5-MAY-1994
PRIOR APPLICATION NUMBER: US 07/872,646
FILING DATE: O8-JUN-1992
PRIOR APPLICATION NUMBER: US 07/715,181
FILING DATE: O8-JUN-1992
PRIOR APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
PRIOR APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
PRIOR APPLICATION NUMBER: US 07/715,181
FILING DATE: 04-DEC-1989
PRIOR APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989
ATTORREY/AGENT INPORMATION:
NAME: KURT G. BEISCOGE
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.7-KG
TELECOMMUNICATION:
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TELEFAX: (914) 332-1844
INPORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 294 amino acids
amino acid
                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear
US-08-468-576B-18
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Sequence 18, Application US/08468577B

Patent No. 601804

GENERAL INFORMATION:
APPLICANT: Rabin, Daniel

ITILE OF INVENTION: DANCREATIC ISLET CELL ANTIGENS

TITLE OF INVENTION: DANCREATIC ISLET CELL ANTIGENS

CORRESPONDENCES:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road

CITY: Tarrytown

STATE: New York

COUNTRY: USA

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COMPUTRY: USA ZIP: 1054

COMPUTRY: USA ZIP: 1054-514

COMPUTRY: USA SYSTEM: APPIEM MCDINCOM, 1.4 Mb storage COMPUTER: APPIEM MCDINCOM, 1.5 0 inch, 1.4 Mb storage COMPUTER: APPIEM MCDINCOM, 1.5 0 inch, 1.4 Mb storage COMPUTER: APPIEM MCDINCOM, 1.5 0 inch, 1.4 Mb storage SOFTWARE: WCATGAFFER CONTROL NATH. System 7.5 SOFTWARE: WCATGAFFER COUNTRY: 0.6 -UN-1995

CLASSIPICATION DATA: APPIEMATION DATA: APPIEMATION DATA: APPIEMATION NUMBER: US 07/872,646

FILING DATE: 0.6 -UN-1992

RELING DATE: 0.6 -UN-1992

RELING DATE: 1 d -UN-1991

PRIOR APPLICATION DATA: APPIEMATION NUMBER: US 07/715,181

FILING DATE: 1 d -UN-1991

PRIOR APPLICATION DATA: APPIEMATION NUMBER: US 07/715,181

FILING DATE: 1 d -UN-1991

PRIOR APPLICATION DATA: APPIEMATION DATA: APPLICATION 
PRICR APPLICATION DATA:

APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
PRICR APPLICATION NUMBER: US 07/441,703
FILING DATE: 04-DEC-1989
PRICR APPLICATION NUMBER: US 07/411,703
FILING DATE: 04-DEC-1989
PRICR APPLICATION DATA: 0807/312,543
PRILING DATE: 17-EBE-1989
ATTORNEY/AGENT INFORMATION:
NAME: KURT G. BTISCOG
REGISTRATION NUMBER: 33,441
REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
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), ORGANISM: Homo sapiens
US-10-038-686-3
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LENGTH: 979
TYPE: PRT
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Sequence 41, Appl
Sequence 40, Appl
Sequence 40, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 52, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
                                                                                                                                October 28, 2004, 11:39:31; Search time 47.4217 Seconds (without alignments) 164.085 Million cell updates/sec
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(gnz_6/prodata/2/pubpaa/USO7_PUBCOMB.pep;*

(gnz_6/prodata/2/pubpaa/USO6_NEW_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO6_NEW_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO6_NEW_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO7_NEW_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO8_NEW_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO8_NEW_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO8_NEW_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO8_PUBCOMB.pep;*

(gnz_6/prodata/2/pubpaa/USO8_PUB.pep;*

(gnz_6/prodata/2/pubpaa/USO8_PUB.pep;*
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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| US-10-038-686-3
| US-10-378-479-42
| US-10-378-479-46
| US-10-378-479-38
| US-10-378-479-38
| US-10-378-479-39
| US-10-378-479-39
| US-10-124-089-4
| US-09-8676-527-4
| US-10-124-089-7
| US-09-876-527-4
| US-10-124-089-7
| US-09-876-527-4
| US-10-124-089-7
| US-09-876-527-4
| US-10-124-089-7
| US-10-124-089-7
| US-10-124-089-7
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24
1 KLKVESSPSRSDYINASPIIEHDP
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Gapop 60.0 , Gapext 60.0
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Perfect score:
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No.
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Sequence 22, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 30320, A
Sequence 219467,
Sequence 219467,
Sequence 94, Appl
Sequence 94, Appl
Sequence 97, Appl
Sequence 67, Appl
Sequence 27, Appl
Sequence 27, Appl
Sequence 11, Appl
Sequence 17, Appl
Sequence 124, Appl
Sequence 124, Appl
  US-09-876-527-22

4 US-10-124-089-22

4 US-10-124-089-16

4 US-10-124-089-16

4 US-10-124-089-16

5 US-10-124-599-19467

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10S-09-788-626-197

10S-09-188-626-197

10S-09-188-626-197

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10S-09-188-626-197

10S-09-188-626-197

10S-09-188-626-197
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Gaps Query Match
Best Local Similarity 100.0%; Pred. No. 2.2e-15;
Matches 24; Conservative 0; Mismatches 0; Indels (USECULE 10-018-686-3

Sequence 3, Application US/10038686

Publication No. US20030045467A1

GENERAL INFORMATION:
TITLE OF INVENTION: AUTOMATIGEN VACCINE
FILE REFERENCE: 10276-067001

CURRENT APPLICATION NUMBER: US/10/038,686

CURRENT FILING DATE: 2002-05-31

PRIOR APPLICATION NUMBER: 60/260,068

PRIOR FILING DATE: 2001-01-05

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FASTSEQ for Windows Version 4.0 1 KLKVESSPSRSDYINASPIIEHDP 24

KIKVESSPSRSDYINASPIIEHDP 775

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RESULT 2
US-10-378-479-41
US-10-378-479-41
Sequence 41, Application US/10378479
Publication No. US20040006202A1
GENERAL INFORMATION
APPLICANT: Peakman, Mark
APPLICANT: Chicz, Roman M.

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US-10-378-479-40
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US-10-378-479-38
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TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROWOTING
TITLE OF INVENTION: C04+ T LYMPHOCYTES
FILE REFERENCE: 08191-009002
CURRENT APPLICATION NUMBER: US/10/378,479
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US/09/552,802B
PRIOR APPLICATION NUMBER: US 09/295,868
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR FILING DATE: 1999-04-21
PRIOR SEDICATION NUMBER: US 60/130,355
PRIOR FILING DATE: 1999-04-21
SEQ ID NOS: 55
SOFTWARE: FastEEQ for Windows Version 4.0
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Sequence 42, Application US/10378479

Publication No. US20040006202A1

GENERAL INFORMATION:
APPLICANT: Peakman, Mark

APPLICANT: Peakman, Mark

APPLICANT: Peakman, Mark

TITLE OF INVENTION: EPPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING

TITLE OF INVENTION: CD4+ T LYMPHOCYTES

TOURRENT PILING DATE: 2003-03-03

PRIOR PILING DATE: 1999-04-21

PRIOR APPLICATION NUMBER: US 60/130,355

PRIOR PILING DATE: 1999-04-21

PRIOR PILING DATE: 1999-04-21

NUMBER OF SEQ ID NOS: 55

SEQ ID NO 42

SEQ ID NO 42

LENGTH: 19
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Publication No. US20040006202A1
GENERAL INFORMATION:
APPLICANT: Peakeman, Mark
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: DEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
FILE 'REFERENCE: 08191-009002
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Pred. No. 7.8e-15;
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Pred. No. 6.2e-12;
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100.0%; Pred
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US-10-378-479-41
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; ORGANISM: Homo sapiens
US-10-378-479-42
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Best Local Similarity
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Sequence 38, Application US/10378479

PUDLication No. US20040006202A1

GENERAL INFORMATION:
APPLICANT: Peakman, Mark
APPLICANT: Chicz, Roman M.
ITLLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
ITLLE OF INVENTION: DEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
ITLLE OF INVENTION: DEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
ITLLE OF INVENTION: DEAH INVENTION: US4 T LYMPHOCYTES
CURRENT APPLICATION NUMBER: US/10/378,479
CURRENT APPLICATION NUMBER: US/09/552,802B
PRIOR APPLICATION NUMBER: US 09/295,868
PRIOR PLING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/130,355
PRIOR PRIOR DATE: 1999-04-21
PRIOR PLING DATE: 1999-04-21
PRIOR PLING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/130,355
PRIOR PLING DATE: 1999-04-21
PRIOR PLING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/130,355
PRIOR PLING DATE: 1999-04-21
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Publication No. US20040006202A1

GENERAL INFORMATION:
APPLICANT: Peakman, Mark
APPLICANT: Peakman, Mark
APPLICANT: Peakman, Mark
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
TITLE OF INVENTION: CD4+T LYMPHOCYTES
FILE REFERENCE: 08191-009002
CURRENT APPLICATION NUMBER: US/10/378,479
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US/09/552,802B
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CURRENT APPLICATION NUMBER: US/10/378,479
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US/09/552,802B
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 1999-04-21
PRIOR APPLICATION NUMBER: US 60/130,355
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 55
SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 40
LENGTH: 17
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Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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AR09458B Sequence
BC064020 Mus muscu
BT006975 Homo sapi
BT007693 Synthetic
AK122679 Homo sapi
D45414 Rat mRNA fo
AF332084 Mus muscu
AF075170 Bos tauru
                                                                         X92563 R. norvegicu
CQ71477 Sequence
BC00713 Homo sapi
AR06651 Sequence
AR085262 Sequence
AR085262 Sequence
AR094589 Sequence
AR074589 Sequence
1040652 Rettus norv
CQ812832 Sequence
U11812 Mus musculu
D3822 Rettus Sp.
BC068165 Mus musculu
AX564925 Sequence
BC070634 Homo sapi
AX109 Sequence
AG710953 Homo sapi
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L19893 Homo sapien
AR454532 Sequence
BV106091 MARC 8095
AC114803 Homo sapi
AC160820 Homo sapi
AC161801 Popio anu
AC121001 Rattus no
AC118950 Rattus no
AC118950 Rattus no
BXA47878 Zebrafish
BX23576 Danio rer
EXCO5327 Zebrafish
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BX005327 Zebrafish
BV203767 sgnm21297
AR369581 Sequence
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Kindsvogel, W., Jelinek, L.J., Sheppard, P.O., Hagopian, W.A. and Lagasse, J.M.
Lagasse, J.M.
Patent: US 6300093-A 30 09-OCT-2001,
Location/Qualifiers
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ARQUENCE 30 from patent US 6300093.
AR369579 GI:34605766
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MMUJ1812
RATDDTFLP
BCG68165
AX364925
BCG70053
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BV106091
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AC14918
AC121001
AC106467
AC118950
BX247878
BX323576
BX323576
BX005327
AR369581
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/mol_type="mRNA"
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Pred. No.:
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AR369579
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JOURNAL
FEATURES
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AUTHORS
   ORIGIN
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AR404158 Sequence
AR060650 Sequence
AR085261 Sequence
                                                          October 28, 2004, 16:28:53; Search time 1574.75 Seconds (without alignments) 720.721 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                           nucleic search, using frame_plus_p2n model
                                                                                                                                                                              4526729 segs, 23644849745 residues
                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
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Maximum DB seq length: 200000000
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PAT 01-SEP-2000
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                                                                                                                                          1 LysLeuLysValGluSerSerProSerArgSerAspTyrIleAsnAlaSerProllelle 20
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Rabin,D.U.
Pancreatic islet cell antigens obtained by molecular cloning
Patent: US 5981700-A 9 09-NOV-1999;
Location/Qualifiers
1. 1413
/.rganism="unknown"
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AR085261
AR085261.1 GI:10012031
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AR094588
AR094588.1 GI:10021642
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                                                                                                      US-10-783-095-12 (1-24) x AR060650 (1-1413)
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AR094588
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AR085261
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                                                                                         527 AAACTGAAGGTGGAGAGCAGCCCTTCTCGGAGCGATTACATCAACGCCAGCCCCATTATT
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Kindsvogel, W., Jelinek, L.J., Sheppard, P.O., Hagopian, W.A. and
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Ladasse,J.M...
Ladasse,J.M...
Islet cell antigen 1851
Location/Qualifiers
Location/Qualifiers
1. .1210
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/organism="unknown"
/mol_type="unassigned DNA"
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ARG60650
ARG60650.1 GI:5987100
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Rabin, D.U.
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AR06650
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AR404158
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Add5515 PTPase PT
Add60053 CRH signa
Ab13976 Human NS
Add55970 PTPase PT
Ab199237 Mouse isc
Aax87627 Human isl
Aax68754 Human aut
Aax16873 Fusion pr
Ach14280 Human aut
Aax16873 Fusion pr
Ach14280 Human aut
Aax16873 Fusion pr
Ach14280 Human isl
Aax16529 Human isl
Aax16529 Human isl
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Aax16480 Mouse ins
Aax16480 Mouse ins
Aax164936 Mouse ins
Aax164936 Mouse isl
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Adn95437 Human Brc
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Adi55437 Human pol
Aal44150 Barley ye
Aaz88566 BYDV-PAV
Human pan
Islet cel
Pancreati
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Aaz46460 E
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        AAV63561
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ADO60053
ABT41712
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AAS87633
ACA55641
ADI55437
AAL44150
AAZ88566
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ADP18660
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AA168754
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AA168773
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AAT95229
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05-MAR-1997;
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15-OCT-1996;
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AAT95246
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Aaz09922 Human isl
Aax32241 Human pan
Aav63560 Islet cel
Aax46459 Pancreatii
Aaz09923 Human isl
                                                           October 28, 2004, 16:24:37; Search time 312.578 Seconds (without alignments) 403.055 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Description
         GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                            nucleic search, using frame_plus_p2n model
                                                                                                                                                                                       4134886 seqs, 2624710521 residues
                                                                                                                                                                                                                             parameters
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560.0 , Ygapext 60.0
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AAZ09922
AAZ32341
AAV63560
AAZ46459
AAZ09923
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                                                                                                                                                               This cDNA sequence comprises the cytoplasmic region of human protein tyrosine phosphatase IA-2/ICA512. It was obtained from UB7MG glioblastoma cells (ATCC M85) by PCR amplification (see AAT95244-45). The 1.2 kb product was ligated into pECEP. Sera from prediabetic subjects were screened for IA-2/ICA512 autoantibodies. A novel islet cell antigen, designated 1851 (see AAM32256-97), has been identified that forms an immune complex with an autoantibody found in patients at risk of, or predisposed to, insulin-dependent diabetes mellitus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        527 AAACTGAAGGTGGAGAGCAGCCCTTCTCGGAGCGATTACATCAACGCAGCCCATTATT 586
                      Mammalian pancreatic islet cell antigen and related DNA - used to detect auto:antibodies indicative of insulin-dependent diabetes or predisposition to it.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 LysLeuLysValGluSerSerProSerArgSerAspTyrIleAsnAlaSerProIleIle 20
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/note="Partial sequence, no start codon given"
/product= "ICA-512"
                                                                                                                                                                                                                                                                                                                                                                  Sequence 1210 BP; 245 A; 383 C; 370 G; 212 T; 0 U; 0 Other;
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Matches:
Conservative:
Mismatches:
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                                                                                                                           Example 3; Page 111; 134pp; English
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89US-00441703.
91US-00715181.
92US-00872646.
94US-00239276.
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WPI; 1997-457535/42
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14-JUN-1991;
08-JUN-1992;
05-MAY-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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No.:
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This invention describes novel isolated and purified DNAs encoding pancreatic islet cell antigens reactive with islet cell antibodies found in sear of patients with insulin-dependent type I diabetes mealitus (IDDM). The polypeptides of the invention are useful as immunoassy reagents in the presymptomatic diagnosis of insulin-dependent type I diabetes.mellitus (IDDM). The ability of the polypeptides to bind the artibody binding site on islet cell antibodies (ICAs) also confers utility in the binding or blocking of human immunoglobulin, T-cells, or B cells involved in IDDM. The products can also be used to study the appearance of ICA. The immunoreactivity profile with different antigens can provide diagnostically significant information concerning the nature of the disease, e.g. subtypes, the efficacy of the disease, the proximity to onset of the disease, and the efficacy of therapy, e.g. immune therapy. The antigens can serve as stimulating antigens for T-cell culture, and growth. The availability of large quantities of pure antigen enables the development of highly sensitive and specific immunoassays which can be bredisposition to develop IDDM. This sequence encodes the human islet cell antigen from clone ICA-512
                                                                                                                                                                                                                                 Isolated DNA encoding antigens reactive with serum from diabetics useful to develop products for the diagnosis and monitoring of insulin-dependent diabetes mellitus.
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detection;
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(FARB ) BAYER CORP FORMERLY MOLECULAR DIAGNOSTIC.
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Matches:
Conservative:
Mismatches:
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Best Local Similarity:
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Sequence 1375, Ap
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13160, A
11236, A
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33, Appl
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US-09-248-766A-13160
US-09-513-999C-11236
US-09-702-1375
US-09-736-457-1375
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US-09-671-325-1375
US-09-658-824-1375
US-09-513-999C-32217
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US-09-270-767-11566
US-09-270-767-14755
               US-09-811-481-3
US-09-876-527-3
US-09-876-527-3
US-09-876-527-3
US-09-876-527-6
US-09-876-527-6
US-09-876-527-1
US-09-876-527-1
US-09-811-59-6
US-09-811-59-6
US-09-876-527-1
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US-09-876-527-1
US-09-876-527-1
US-09-876-527-1
US-09-876-527-1
US-09-876-527-1
US-09-876-527-23
US-09-548-159-2
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US-09-016-434-239
US-09-984-863-2
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 30, Application US/08811481
Patent No. 6300033
GENERAL INFORMATION:
APPLICANT: Kindsvogel, Wayne
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Hadasse, James M.
APPLICANT: Ladasse, James M.
TITLE OF INVENTION: ISSET CELL ANTIGEN 1851
                                                                                                                                                                                                                                                                                                                                                                                       US-08-884-569A-1
US-08-811-481-15
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ER: 95-36
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REGISTRATION NUMBER: P-41,15
REFERENCE/DOCKET NUMBER: 95-
TELECOMMUNICATION INFORMATION:
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: ISLI
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymoGenetic
STREET: 1201 Eastlake
CITY: Seattle
                                                                   \begin{array}{c} 111111\\ 11111\\ 120202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 20200\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020\\ 202020
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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US-08-811-481-30
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-MODEL=frame+ parameters:
-MODEL=frame+ par.model -DEV=xlp
-MODEL=frame+ par.model -DEV=xlp
-G=Cgn2_1/USFTO_spool_p/USIO783095/runat_26102004_185455_25065/app_query.fasta_1.796
-D=-Cgn2_1/USFTO_spool_p/USIO783095/runat_2611.rni -MINMATCH=0.1 -LOOPCL=0
-DEV=SENCE Parents NA -OFTMR=T=1 -END=-1 -MATRIX=01190 -TRANS=human40.cdi
-LISTA=5 -DOCAMIGN=200 -THR SCORE-quality -THR MIN=1 -ALIGN=15 -MODE=LOCAL
-USFR=45 -DOCAMIGN=200 -THRPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USIO783095 @CGN 1 1_213 @runat_26102004_185455_25065 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NGS_CSCRES=0 -MAIT -DSPBLOCK=100 -LONGLOG
-DSV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPEXT=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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Sequence 30, Appl
Sequence 9, Appli
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Sequence 10, Appl
Sequence 11, Appl
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Sequence 21, Appli
Sequence 5, Appli
Sequence 5, Appli
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/PcTUS_COMB.seq:*
                            GenCore version 5.1.6
(c) 1993 - 2004 Compugen Ltd.
                                                                                                                        - nucleic search, using frame_plus_p2n model
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US-09-876-527-30
US-08-23-276-9
US-08-468-579B-9
US-08-468-577B-9
US-08-468-577B-10
US-08-468-577B-10
US-08-577B-10
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24
1 KLKVESSPSRSDYINASPIIEHDP 24
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0
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seg length: 200000000
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Maximum DB
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TYPE: nucleic
STRANDEDNESS:
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ZIP: 98102
COMPUTER READABLE FORM:
MUDELUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
CONFUTING SYSTEM: DOS
SOTTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,527
FILING DATE: 07-Jun-2001
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/811,481
FILING DATE: -Unknown>
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: P-41,156
REPERSINGE/DOCKET NUMBER: 95-36
THIRCANTING CRATICN NUMBER: P-41,156
REPERSINGE/DOCKET NUMBER: 95-36
THIRCANTINGENITON: NEORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 30, Application US/09876527

Patent No. 6627735

GENERAL INFORMATION:

APPLICANT: Kindsvogel, Wayne

Jelinek, Laura J.

Sheppard, Paul O.

Hagopian, William A.

ITILE OF INVENTION: ISLET CELL ANTIGEN 1851

NUMBER OF SEQUENCES: 34

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Zymcdenetics, Inc.

STREET: 1201 Eastlake Avenue East

CONTY: Seattle
                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                             US-10-783-095-12 (1-24) x US-08-811-481-30 (1-1210)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 206-442-6678
TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS.
LENGTH: 1210 base pairs
TYPE: nucleic acid
                                                               INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 1210 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
1.52e-15
                                                                                                                                                                                                                                                                   24.00
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100.00%
100.00%
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                                                                                                                                                                       MOLECULE TYPE: CDNA
US-08-811-481-30
                                                                                                                                                             linear
                                                                                                                                                                                                                                                                               Percent Similarity:
Best Local Similarity:
Query Match:
DB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: WA
                                                                                                                                                                                                                               Alignment Scores:
                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-876-527-30
                                                                                                                                                                                                                                                    Pred. No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 2
                                                                                                                                                                                                                                                                     Score:
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527 AAACTGAAGGTGGAGGAGCCCTTCTCGGAGCGATTACATCAACGCCAGCCCCATTATT 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Tarrytown STATE: New York COMPUTRY: USA ZIP: 10591-5144

ZIP: 10591-5144

ZIP: 10591-5144

COMPUTRY: Apple Macintcsh OPERATING SYSTEM: System 7.5

SOFTWARE: Macheriect COMPUTRY: Macheriect CURRENT APPLICATION DATA: DATE: 04-DEC-1989

PRIOR APPLICATION DATA: US 07/312,543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 9, Application US/08239276
Patent No. 5840836
GENERAL INFORMATION:
ADDITION RABIN, Daniel
TITLE OF INVENTION: DANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSE: Sprung Kramer Schaefer & Briscoe
STREET: 660 White Plains Road
CITY: Tarrytown
STATE: New York
                                                                                                                                                                                             Length:
Matches:
Conservative:
Mismatches:
Indels:
Gaps:
                                                                                                                                                                                                                                                                                                                                                                                  US-10-783-095-12 (1-24) x US-09-876-527-30 (1-1210)
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FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: KURT G. BLISCOE
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: MDI 251.4-KGB
TELECOMMUNICATION INFORMATION:
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-09-876-527-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1413 nucleotides
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                                                                                                                                                                                                                                    Percent Similarity:
Best Local Similarity:
Query Match:
DB:
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Perfect score:

Run on:

Sequence:

Scoring table:

Word size:

Searched:

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Sequence 31, App 1, Sequence 32, App 1, Sequence 33, App 1, Sequence 33, App 1, Sequence 33, App 1, Sequence 6, App 1, Sequence 6, App 1, Sequence 1, App 1, Sequence 23, App 1, Sequence 23, App 1, Sequence 23, App 1, Sequence 23, App 1, Sequence 24, App 1, Sequence 275, App 2, App 2, App 2, App 3, App 2, App 2, App 3, App 3, App 2, App 3, App 4, Ap
                                                      Sequence 30, Appl
Sequence 30, Appl
Sequence 167, App
Sequence 1414, Ap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1375, Ap
Sequence 1375, Ap
Sequence 1375, Ap
Sequence 1375, Ap
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Sequence 75067, A
Sequence 76625, A
                                           15 US-00-876-527-30

16 US-10-124-089-30

16 US-10-124-089-30

17 US-10-1175-523-167

18 US-09-918-995-1492

19 US-09-918-995-1492

19 US-09-918-995-1492

19 US-09-876-527-3

19 US-09-876-527-3

19 US-09-876-527-3

19 US-09-876-527-1

10 US-10-124-089-1

10 US-10-124-089-1

11 US-10-124-089-1

12 US-10-124-089-1

13 US-10-124-089-1

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16 US-10-124-089-1

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18 US-10-124-089-1

19 US-09-876-527-1

10 US-10-124-089-1

11 US-10-124-089-1

12 US-10-124-089-1

13 US-10-124-1

14 US-10-127-132-148982

16 US-10-127-137-1

16 US-10-127-137-1

17 US-10-127-137-1

18 US-10-127-137-1

19 US-09-84-663-1

10 US-09-94-663-1

11 US-10-127-137-1

11 US-10-127-137-1

12 US-09-849-621-137-1
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| Patent No. US20020102616A1
| GENERAL INFORMATION:
| APPLICANT: Kindsvogel, Wayne
| APPLICANT: Kindsvogel, Wayne
| Happard, Paul O. Happard, William A. Infer OF INVENTION: ISLET CELL ANTIGEN 1851
| NUMBER OF SEQUENCES: 34
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ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue
CITY: Seattle
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COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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                                                                                                                                                                                           October 28, 2004, 22:07:29; Search time 1265.93 Seconds. (without alignments) 97.211 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Applications NA:*

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2: /cgn2_6/ptodata/1/Pubpna/DCT_NW PUB.seq:*
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21: /cgn2_6/ptodata/1/Pubpna/US10B_PUBCOMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                              OM protein - nucleic search, using frame_plus_p2n model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3413475 segs, 2563800928 residues
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                                                                                                                                                                                                                                                                                                                                                                                                 KLKVESSPSRSDYINASPIIEHDP 24
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, Ygapext 6
, Fgapext
, Delext
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Maximum DB seq length: 200000000
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24
1 KLKVESSPSRSDYII
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Xgapop
Ygapop
Fgapop
Delop
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Database

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Alignment Scores:
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COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FESTEM: DOS
SOFTWARE: FESTEM: DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/876,527
FILING DATE: O'-Jun-2001
FILING DATE: O'-Jun-2001
PRIOR APPLICATION NUMBER: 08/811,481
APPLICATION NUMBER: 08/811,481
ATTORNEY/ACENT INFORMATION:
NAME: Lingenfelter, Busan
REGISTRATION NUMBER: 95-36
TELERENCE/DOCKET NUMBER: 95-36
TELERENCE/DOCKET NUMBER: 95-36
TELERENCE/OFGT NUMBER: 95-36
TELERENCE/
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ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: SYSTEM: DOS
SOFTWARE: FastSEQ_for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
Matches:
Conservative:
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Indels:
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TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
RADBRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-783-095-12 (1-24) x US-09-876-527-30 (1-1210)
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APPLICATION NUMBER: US/10/124,089
FILING DATE: 16-Apr-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TOPOLOGY: linear; MOLECULE TYPE: CDNA; SEQUENCE DESCRIPTION: SEQ ID NO: 30: US-09-876-527-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 30, Application US/10124089
; Publication No. US20030166067A1
; GENERAL INFORMATION:
    APPLICANT: Kindsvogel, Wayne
    Jelinek, Laura J.
Sheppard, Paul O.
Hagopian, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1210 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.00%
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STATE: WA
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 2
US-10-124-089-30
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Sequence 167, Application US/10175523
Publication No. US200300962441
GENERAL INFORMATION:
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Jeffrey
APPLICANT: Brockman, Michael
APPLICANT: Balfreyman, Michael
APPLICANT: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               527 AAACTGAAGGTGGAGGAGCCCTTCTCGGAGCGATTACATCAACGCCAGCCCCATTATT 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 LysLeuLysValGluSerSerProSerArgSerAspTyrIleAsnAlaSerProIleIle 20
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Matches:
Conservative:
Mismatches:
Indels:
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CLASSIFICATION: <......

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/811,481

FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:

NAME: Lingenfelter: Susan

REGISTRATION NUMBER: P-41,156

TELEPRONES/DOCKET NUMBER: 95-36

TELEPRONE: 206-442-6675

TELEPRONE: 206-442-6678

TELEPRONE: 206-442-6678

TELEPRONE: 206-442-6678

TELEPRONE: 206-442-6678

TELEPRONE: CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 1210 base pairs

"TOTAL DASE DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 30:
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100.00%
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Best Local Similarity:
Query Match:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using
search,
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October 28, 2004, 11:13:10; Search time 12.4337 Seconds (without alignments) 185.721 Million cell updates/sec Run on:

Perfect Title:

24 US-10-783-095-12 24 1 KLKVESSPSRSDYINASPIIEHDP score: Sequence:

OLIGO Scoring table: 283416 seqs, 96216763 residues Searched:

Gapop 60.0 , Gapext 60.0

Word size

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

piri: piri: pir3:* *:64

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1		مد (
No.	Score	Match	Length	DB	Ω	Description
-	24	. 0	548	. 4	I37577	islet cell antiden
N	24	ö	922	H	S54342	otein-tyrosi
m	24	00	979	Н	4.	
4	24	00	966	7	148721	PTP 35 protein - m
'n	σ	۲.	248	(7	T46903	hypothetical prote
w	σι	ζ.	1015	7	JC5062	Sor
7	σ	۲.	1015	N	C52	transmembrane tyro
œ	7	φ.	113	N	F90464	hypothetical prote
σ	7	9	211	0	G90209	the
10	7	φ.	377	Н	A48711	vrosine-
11	7	φ.	397	0	T11777	ø
12	7	φ.	397	N	AI0806	phosphoglycerate t
13	7	6	398	(1)	I56540	protein-tyrosine-p
14	7	6	477	N	I38409	cyclase-
15	7	ę.	519	Ŋ	T48498	hypothetical prote
16	7	o,	582	IJ	A57068	protein-tyrosine-p
17	7	φ.	583	N	S17671	protein-tyrosine-p
18	7	6.	668	7	Н	ne-
19	7	ď	680	(1	\circ	tyros
20	7	σ.	669	(1	JC6132	-tyrosine-
21	7	σ.	700	Н	\circ	-tyrosine-
22	7	σ,	711	Н	m	ne-
23	7	ď	711	~	-	-tyrosine-
24	7	ο,	756	7	867433	rot
22	7	σ.	796	Н	JC1285	protein-tyrosine-p
56	7	ω,	802	н	A36065	ne-
27	7	ω.	829	Н	A47373	ine-
28	7	29.5	839	7	8469	hypothetical prote
9	7	σ.	1118	Н	A49724	protein-tyrosine-n

probable protein-t	protein-tyrosine-p	protein-tyrosine-p	leucocyte common a	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	probable protein-t	protein-tyrosine-p	protein-tyrosine-p	protein-tyrosine-p	leukocyte antigen-	leukocyte antigen-	protein-tyrosine-p	protein-tyrosine-p
T43148	S53089	A54080	A56493	A41622	A48758	I50212	158148	T19121	D54689	846217	C54689	TDHULK	S46216	S50893	A56178
(7)	0	~1	7	н	۲-4	~	~	7	-	ď	~	-	~	N	N
1200	1231	1237	1290	1301	1496	1499	1501	1585	1691	1863	1894	1897	1898	1907	1912
29.5	29.5	29.5	29.5	29.5	29.5	29.5	29.5	29.5	29.5	29.5	29.2	29.5	29.5	29.5	29.2
7	7	7	7	7	7	7	7	۲-	7	7	۲-	7	7	7	7
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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NyAlternate names: islet cell autoantigen 3
NyAlternate names: islet cell autoantigen (EC 3.1.3.48)
CyBecies: Home sapiens (man)
CyBecies: Home sapiens (man)
CyBecies: Howe sapiens (man)
CyBecies: Howe sapiens
CyBecies: Howe sapiens
CyBecies: Howe sapiens
CyBecies: No. 1912
CyBecies: No. 1913
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A;Cross-references: GDB.185512
A;Cross-references: GDB.185512
A;Cross-references: GDB.185512
A;Cross-references: GDB.185512
C;Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphata C;Keywords: phosphoprotein; phosphoric monoester hydrolase; transmembrane protein; tyros F;196-212/Domain: transmembrane #status predicted <TMN>
F;186-548/Domain: protein-tyrosine-phosphatase homology #status atypical <PTP>
F;521/Active site: Cys (phosphocysteine intermediate) #status predicted
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Best Local Similarity 100.0
Matches 24; Conservative
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KLKVESSPSRSDYINASPITEHDP 387 1 KLKVESSPSRSDYINASPIIEHDP 24 364 à g

Cydace: 10.554342

R; Kambayashi, Y.; Takahashi, K.; Bardhan, S.; Inagami, T.

Biochem. J. 306, 331-332, 1995

A; Title: Cloning and expression of protein tyrosine phosphatase-like protein derived from A; Reference number: S54342; MUID:95194305; PMID:7887886

A; Accession: S54342

A; Accession: S54342

A; Molecule type: mRNA

A; Molecule type: mRNA

A; Residues: 1-922 < KRNA

A; Residues: 1-922 < KRNA

A; Cross-references: GB:D38222; NID:91504061; PIDN:BAA07397.1; PID:9808890

C; Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphata procein-tyrosine-phosphatase (BC 3.1.3.48), receptor type N precursor - rat NAlternate names: protein-tyrosine-phosphatase IA-2 (Species: Rattus norvegious (Norway rat C.Species: Rattus norvegious (Norway rat C.Species: Bernales: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000

monoester hydrolase; transmembrane protein; tyros

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C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A,Accession: T46903
A,Status: preliminary
A,Molecule type: mRNA
A,Residues: 1-248 <AAA>
                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                  protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type N precursor - mouse N;Alternate names: protein-tyrosine-phosphatase IA-2 (Species: Mus musculus (house mouse) (C)Species: Mus musculus (house mouse) (C)Accession: 0.5ep-1999 #text_change 09-Jul-2004 (C)Accession: 0.72349; S40291; I48721 (S)Lu, J.; Notkins, A.L.; Lan, M.S. (S)Comban. 204, 930-936, 1994 (S)Comban. 204, 930-936, 19960563
                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
        C,Keywords: phosphoprotein, phosphoric monoester hydrolase, transmembran F;525-541/Domain: transmembrane #status predicted <TWM> F;67-901/Domain: protein-tyrosine-phosphatase homology <PTF2> F;677-901/Domain: protein-tyrosine-phosphatase homology <PTF2> F;852/Active site: Cys (phosphocysteine intermediate) #status predicted F;858/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;734-958/Domain: protein-tyrosine-phosphatase homology <PTP2>
F;506,524/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;909/Active site: Cys (phosphocysteine intermediate) #status predicted
F;915/Binding site: substrate phosphate (Arg) #status predicted
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1148721
PTP 35 protein ~ mouse
C;Species: Mus musculus (house mouse)
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                                                                                                                                                                  Conservative
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Best Local Similarity
Matches 24; Conserv
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Rymagistrelli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
Rymagistrelli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
Rymagistrelli, G.; Covinin, N.; Mosca, M.; Lippoli, G.; Isacchi, A.
Biochem. Biophys. Res. Commun. 127, 134-161, 1995

A; Reference number: 148721; MUD: 96095652; PMID: 8526904

A, Reference number: 148721

A, Reference number: 148721; MUD: 96095652; PMID: 8526904

A, Status: preliminary; translated from GB/EMBL/DDBJ

A, Residues: 1-996 ex RES>
A, Residues: 1-996 ex RES>
A, Residues: 1-996 ex RES>
C, Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatase
C, Keywords: phosphoprotein
F; 751-975/Domain: protein-tyrosine-phosphatase homology express
F; 926/Active site: Cys (phosphocysteine intermediate) #status predicted
F; 932/Binding site: substrate phosphate (Arg) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N.Contains: protein-tyrosine-phosphatase (EC 3.1.3.48) receptor type (Species: Homo sapiens (man) (man) (Contains: Jacoba 1997 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004 (C.) Date: 31-Jan-1997 #sequence revision 31-Jan-1997 #text_change 09-Jul-2004 (C.) Accession: JC5062; JC5563; T46903 R; Kawasaki, E.; Hutton, J.C.; Eisenbarth, G.S. Biochem Biophys. Res. Commun. 27, 440-447, 1996 A; Title: Molecular cloning and characterization of the human transmembrane protein tyrosi A; Reference number: JC5062; MUID:97032784; PMID:8878534
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A,Residues: 1-1015 <KAW>
A,Cross-references: UNIPROT.092932; GB:U66702; NID:g1620663; PIDN:AAC50742.1; PID:g162066
A,Cross-references: UNIPROT.092932; GB:U66702; NID:g1620663; PIDN:AAC50742.1; PID:g162066
R;Smith, P.D.; Barker, K.T.; Wang, J.; Lu, Y.J.; Shipley, J.; Crompton, M.R.
Biochmen Biophys. Res. Commun. 229, 402-411, 1996
A,Title: ICAAR, a novel member of a new family of transmembrane, tyrosine phosphatase-li}
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A;Experimental source: adult amygdala; clone DKFZp761A0712
Genetics:
A;More: DKFSzp761A0712.1
C;Superfamily: protein-tyrosine-phosphatase, receptor type N; protein-tyrosine-phosphatas
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C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: T4509
R;Ansorge, W.; Wirkner, U.; Mewes, H.W.; Weil, B.; Wiemann, S.
Submitted to the Protein Sequence Database, February 2000
A;Reference number: Z24134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 24; DB 2; I 100.0%; Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Best Local Similarity 100.
Matches 9; Conservative
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmamalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 330)

2 Akimura,T., Arakawa,T., Carninci,P., Furuno,M., Hanagaki,T.,

Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Imotani,K.,

Ishii,Y., Ito,M., Kawai,J., Kojima,Y., Konno,H., Kouda,M.,

Matsuyama,T., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R.,

Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sakazume,N.,

Sagabe,Y., Sutuki,H., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,

Tanaka,T., Tomaru,A., Toya,T., Watahiki,A., Yasunishi,A.,

Muramatsu,M. and Hayashizaki,Y.

RIKEN Encyclopedia of Mouse Full-length CDNAS (Akimura,T., et al.
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The Institute of Physical and Chemical Research (RIKEN)
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Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/
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249365 MA
ih25h03.y
ud59a10.r
2111-31 M
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CB695128 AMGNNUC: N
CB741393 AMGNNUC: N
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CA541452 C0608605-
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                                                                                  October 28, 2004, 19:58:09; Search time 2727.04 Seconds (without alignments) 320.697 Million cell updates/sec
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Copyright (c) 1993 - 2004 Compugen Ltd.
                                                        nucleic search, using frame_plus_p2n model
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Ygapop 60.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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    /organism="Rattus norvegicus"
/mol_type="mRNA"

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Contact: Dan Fitzpatrick
Amgen, Inc
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Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)

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Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara, Y. and Hayashizaki, Y.

Computer-based methods for the mouse full-length cDNA computer-based methods for the full-length cDNA computer-based methods for the mouse full-length cDNA computer-b
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Smith,T.P.L., Grosse,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,
Casas,E., Wary,J.E., White,J., Cho,J., Fahrenkrug,S.C.,
Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,
Chitko-McKown,C.G., Pertea,G., Holt,I., Karamycheva,S., Liang,F.,
Quackenbush,J. and Keele,J.W.
Sequence evaluation of four pooled-tissue normalized bovine CDNA
libraries and construction of a gene index for cattle
Genome Res. 11 (4), 626-630 (2001)
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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/clone lib="RKEN full-length enriched, 16 days neonate
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397 bp mRNA linear EST 16-MAY-2003
AMGNNUC:TRPA3-00011-D3-A trpa3 (10298) Rattus norvegicus CDNA clone
trpa3-00011-d3 5', mRNA sequence.
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smithGemail.marc.usda.gov
Email: smithGemail.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
vo.980904.e. vector identified by cross_match with the -minscore 18
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Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
/note="vector: pCMV spoRT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from lymph node, ovary,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
Matches:
Conservative:
Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels:
                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/mol_type="mkNA"
/db_xref="taxon:9913"
/iisue_type="pooled"
/lab_host="DH108"
```

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.
```

OM protein - protein search, using sw model

October 28, 2004, 10:57:30; Search time 60.7229 Seconds (without alignments) 227.410 Million cell updates/sec Run on:

US-10-783-095-12 24 1 KLKVESSPSRSDYINASPIIEHDP 24 Title: Perfect score: Sequence:

OLIGO Gapop 60.0 , Gapext 60.0 Scoring table:

1825181 segs, 575374646 residues Searched:

0

Word size :

1825181 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description .	Adhe4020 mus musculu Aah64020 mus musculu Aah64020 mus musculu Qy561a0 homo sapien Q95516 mus musculu Q92516 mus musculu Q92516 mus musculu Q92516 mus musculu Q61849 homo sapien P6672 bos taurus Q65229 rattus norv Q66229 rattus norv Q65229 rattus norv Q65229 rattus norv Q65229 rattus norv Q55416 homo sapien Q94416 homo sapien Q94416 homo sapien Q94416 homo sapien Q95232 homo sapien Q95232 homo sapien Q95232 homo sapien Q9534 canis rattus norv Q02695 macaca neme Q95931 homo sapien Q959416 homo sapien Q99416 gallus gall Q90951 gallus gall Q90951 gallus gall Q90951 gallus gall
SUMMARIES	Q6PBE AAH64020 CYKZ84 C9CKZ84 C9CKZ84 C9CKZ84 C9CKZ84 C9CKZ87 C9CSJT C9CSSJT
DB	
Length	358 358 358 358 361 358 361 361 361 361 361 361 361 361 361 361
5.0	000000000000000000000000000000000000
Score	 - מממטמטמטמטמטמטטטטטטטטטטטטטטטטטטטטטטטט
Result No.	

Q84511 bacillus me Q9usb5 schizosacch Q65476 rattus norv G65928 debaryomyce Q75642 ashbya gos Aa5599 ashbya go Q80fij6 vibrio vuln P34138 dictyosteli Q92052 brachydanio Q80355 brachydanio Q80355 brachydanio Q804055 culicoides Qmmno vibrio vuln P37591 salmonella Q62604 rattus norv
Q84511 Q9USBS Q9USBS Q63476 Q63476 Q65YAB AASO0599 Q8DFJC CXA7_BRARE Q8035 Q8035 Q8MTNO Q7MUG PGTC_SALTY
аааааааааааа
22222222222222222222222222222222222222
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### ALIGNMENTS

Matches

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EQUARMOLE FROM N.A.

Xalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Zhan X., Rolfs A., Halleck A., Hines L., Eisenstein S., Koundinya M., Farmer A.;

Xa Roundinya M., Farmer A.;

Xa Submitted (Max-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, BWBL, BT006975; AAP35621.1; -

RRBJ, BT006975; AAP35621.1; -

RRBJ, BT006975; AAP35621.1; -

RRBJ, PR006975; APPC_motif.

InterPro; IPR000395; PTPC_motif.

R InterPro; IPR000395; TYR_PPosphatase.

R InterPro; IPR000395; TYR_PPosphatase.

R RMRT; SM00194; PTPC; 1.

R RMRT; SM00194; PTPC; 1.

R RMRT; SM00194; PTPC; 1.

R RNGSITE; PS00383; TYR_PHOSPHATASE 1; 1.

R PROSITE; PS00385; TYR_PHOSPHATASE 2; 1.

R PROSITE; PS00385; TYR_PHOSPHATASE PTP; 1.
                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                    Protein tyrosine phosphatase, receptor type, N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 364 KLKVESSPSRSDYINASPIIEHDP 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KLKVESSPSRSDYINASPIIEHDP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase; Receptor.
SEOUENCE 591 AA; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q96IA0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Q961A0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RC STRAINE-EVB/N; TISSUE=Colon;

RX STRAINE-EVB/N; TISSUE=Colon;

RX Strausberg R.L.; Peingold E.A.; Grouse L.H.; Derge J.G.;

REALUSDER R.D.; Peingold E.A.; Grouse L.H.; Derge J.G.;

RA Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Altschul S.F.; Joederg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

RA Diatchenko L., Marusina K., Parmer A.A.; Rubin G.M.; Hong L.;

RA Stapleton M.J.; Usdin T.B.; Toshiyuki S., Carninol P., Prange C.;

RA Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

RA Bosak S.A.; McEwan P.J.; McKernan K.J.; Malek J.A.; Gunaratne P.H.;

RA Schards S., Worley K.C.; Hale S., Garcia A.M.; Gay L.J.; Hulyk S.W.;

RA Willalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

RA Pahey J., Helton E., Ketteman M.; Madan A., Rodrigues S., Sanchez A.,

RA Rodriguez A.C.; Grimwood J., Schmutz J., Dickson M.C.;

RA Rodriguez A.C.; Grimwood J., Schmutz J., Myers R.M.;

Jones S.J.; Marra M.A.;

RA Rodriguez A.C.; Marra M.A.;

RA Gones S.J.; Marra M.A.;

RA Gones S.J.; Marra M.A.;

RA Gones S.J.; Marra M.A.;

RA Fro. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                  ..
                                                      100.0%; Score 24; DB 2; Length 358; 100.0%; Pred. No. 2.8e-17; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 24; DB 2; Length 358; 100.0%; Pred. No. 2.8e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strausberg R.; Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases. EMBL; BC064020; AAH64020.1; NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE 358 AA; 40571 MW; 0152828A35992BF2 CRC64;
        NON TER 1 1 1
SEQUENCE 358 AA, 40571 MW, 0152828A35992BF2 CRC64;
                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
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                                                                                                                                                                                                                                                                         358 AA
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              131 KLKVESSPSRSDYINASPITEHDP 154
                                                                                                                                                                        131 KLKVESSPSRSDYINASPIIEHDP 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLKVESSPSRSDYINASPIIEHDP 24
                                                                                                                                      1 KLKVESSPSRSDYINASPIIEHDP 24
                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                         PRT;
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                                                                                                                                                                                                                                                                                                           02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27, 02-MAR-2004 (TrEMBLrel. 27,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=FVB/N; TISSUE=Colon;
                                                                                                                                                                                                                                                                                                                                                               Ptprn protein (Fragment). PTPRN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24; Conservative
                                                                              Local Similarity 100.
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                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                           02-MAR-2004
02-MAR-2004
                                                                                                                                                                                                                                                                                             AAH64020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                              Query Match
                                                                                                                                                                                                                                                                         AAH64020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q7KZS4
Q7KZS4;
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RESULT 2
AAH64020
AAH64020
AAH64020
DT 02-M
DT

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MEDLINE=22388257; PubNed=12477932;

A KIDLINE=2238827; PubNed=12477932;

A Klausher R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Idschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hishe F.,

A Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheefz T.E.,

Brownstein M.J. Usdin T.B., Toshiyuki S., Carnino B.P., Millahy S.J.,

A Baha S.B., Loquellano N.A., Peters G.J., Abramson R.D., Millahy S.J.,

Brownstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,

A Rakesley R.W., Touchman U.W., Green E.D., Dickson M.C.,

A Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

A Rakesley R.W., Touchman J.W., Green E.D., Myers R.W., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryora, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                          ..
0
                                                                                100.0%; Score 24; DB 2; Length 591; 100.0%; Pred. No. 4.5e-17;
                                                                                                                                                                          Indels
64763 MW; 3AD00A900C03FF4F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q961A0;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UTUN-2003 (TrEMBLrel. 24, Last annotation update)
PTPRN protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       811 AA.
                                                                                                                 100.0%; Pred. No.
```

Matches

8

RESULT 3 Q7KZS4 ID Q7KZ AC Q7KZ DT 05-J1 DT 05-J1

```
GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on: October 28, 2004, 06:03:19; Search time 84.7229 Seconds (without alignments)

Title: US-10-783-095-12
Perfect Score: 123
Sequence: 1 KLKVESSPSRSDYINASPIIEHDP 24
Scoring table: BLOSUN62
Gapop 10.0, Gapext 0.5
Searched: 2002273 seqs, 358729299 residues
Total number of hits satisfying chosen parameters: 2002273
```

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

A Geneseq 23Sep04:*

1: geneseqp1980s:*

2: geneseqp2000s:*

3: geneseqp2001s:*

5: geneseqp2001s:*

6: geneseqp2001s:*

7: geneseqp2003s:*

8: geneseqp2003s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

	Description	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	Aay33360 Human isl	Aay49854 Human pan	Aaw80486 Islet cel	Aay49329 Pancreati	Aay59351 Tyrosine		_		Aay49330 Pancreati	Abu04788 Human exp		Abu04792 Human exp	Abu04791 Human exp	Abu04783 Human exp	Abu04785 Human exp	Abu04795 Human exp	Aar45779 PTPase PT	Abu04786 Human exp	Ade56165 Rat Prote	Add45276 Rat Prote	Abb06112 Human NS	Aar49039 PTPase PT	Abu04787 Human exp	Ado60054 CRH signa	Aay06606 Human isl
	ID		AAY33360	AAY49854	AAW80486	AAY49329	AAY59351	AAY33361	AAY49855	AAW80487	AAY49330	ABU04788	ABU04790	ABU04792	ABU04791	ABU04783	ABU04785	ABU04795	AAR45779	ABU04786	ADE56165	ADD45276	ABB06112	AAR49039	ABU04787	ADO60054	AAY06606
	DB	1 1	7	(7)	~	m	ო	0	~	~	ო	9	9	9	9	9	9	9	~	9	1	7	Ŋ	~	9	ထ	N
	Query Match Length		294	294	294	294	379	548	548	548	548	548	548	548	548	591	591	591	916	916	923	923	934	961	196	978	979
۴	Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0		100.0	100.0	100.0		100.0	100.0	100.0	100.0	100.0
	Score	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123	123
	Kesur No.		7	(7)	ო	4	വ	v	7	60	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

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Human	Human	Humar	Human	Mouse	CD4+	CD4+	Human	Type ]	Human	Macaque	Human	Type							
Aag80205	Abu04793	Abu04784	Abu04789	Abu04794	Ade57230	Ade56167	Ade57226	Add45278	Ade57218	Ade57222	Abb57041	Aab30279	Aab30280	Aaw35300	Aaw18093	Aaw35302	Aaw35298	Aaw35297	Aaw18091
AAG80205	ABU04793	ABU04784 .	ABU04789	ABU04794	ADE57230	ADE56167	ADE57226	ADD45278	ADE57218	ADE57222	ABB57041	AAB30279	AAB30280	AAW35300	AAW18093	AAW35302	AAW35298	AAW35297	AAW18091
4	9	Ø	φ	ω	۲	7	7	7	۲	7	Ŋ	m	ო	N	(7)	N	~	7	7
979	979	979	979	979	979	979	979	979	979	979	966	22	19	298	370	376	641	818	876
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	92.7	74.8	74.0	74.0	74.0	74.0	74.0	74.0
123	123	123	123	123	123	123	123	123	123	123	123	114	92	91	91	91	91	91	91
26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

## ALIGNMENTS

RESULT 1  AAX33360  AAX  XX  XX  AAX  XX  AXX  BE  BE  BE  BE  BE  BE  BE  BE  BE
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AAY49849), ATCC 40551 (AAZ32336, encoding AAY49850), ATCC 40552 (AAZ32337, encoding AAY49851), ATCC 40703 (AAZ32338, encoding AAY49852), ATCC 40706 (AAZ32340), ATCC 40706 (AAZ323410), ATCC 40706 (AAZ32341, encoding AAY49854) and ATCC 75030 (AAZ32342, encoding AAY49855). ICA proteins and their peptide fragments can be used in the diagnosis of IDDM and in detecting or blocking human immunoglobulin, Teclls or B-cells involved in IDDM

Length 294;

Sequence 294 AA;

88888888888

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utility in the binding or blocking of human immunoglobulin, T-cells, or B cells involved in IDDM. The products can also be used to study the biological mechanisms involved in islet cell destruction and the appearance of ICA. The immunocactivity profile with different antiques can provide diagnostically significant information concerning the nature of the disease, e.g. subtypes, the state of the disease, the proximity to onset of the disease, and the efficacy of therapy, e.g. immune therapy. The antigens can serve as stimulating antigens for T-cell culture, permitting significantly improved T-cell choing, identification, and growth. The availability of large quantities of pure antigen enables the development of highly sensitive and specific immunoassays which can be used to screen the general population of presymptomatic IDDM or a used to screen the construction of presymptomatic IDDM or a predisposition to develop IDDM. This sequence represents the human islet cell antigen from clone ICA-512
                                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                     Gaps
antibody binding site on islet cell antibodies (ICAs) also confers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, pancreatic islet cell antigen, ICA clone, IDDM, diabetes, insulin dependent type I diabetes mellitus, diagnosis, detection, immunoglobulin, T-cell, B-cell, antibody binding.
                                                                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human pancreatic islet cell antigen ICA-512 ATCC 40706 protein.
                                                                                                                                                                                                                                                                                     100.0%; Score 123; DB 2; Length 294; 100.0%; Pred. No. 2.1e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORP FORMERLY MOLECULAR DIAGNOSTIC.
                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            110 KLKVESSPSRSDYINASPIIEHDP 133
                                                                                                                                                                                                                                                                                                                                                      1 KLKVESSPSRSDYINASPIIEHDP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY49854 standard; protein; 294 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-00441703.
91US-00715181.
92US-00872646.
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                                                                                                                                                                                                                                                                                                                       24; Conservative
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                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAZ32341.
                                                                                                                                                                                                                                                        Sequence 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (FARB ) BAYER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-DEC-1989;
14-JUN-1991;
08-JUN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7-FEB-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rabin DU;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY49854;
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                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                     Pancreatic islet cell antibody antigen; ICA antigen; diagnosis;
treatment; insulin dependent diabetes mellitus; IDDM; autoantibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide antigens from pancreatic islet cells - useful for the detection and treatment of insulin dependent diabetes mellitus.
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100.0%; Score 123; DB 2; Length 2 100.0%; Pred. No. 2.1e-11; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                           Islet cell antibody antigen encoded by clone ICA-512.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         libraries expressing protein fragments
                                                                         110 KLKVESSPSRSDYINASPIIEHDP 133
                                                         1 KLKVESSPSRSDYINASPIIEHDP 24
                                                                                                                                                          AAW80486 standard, protein; 294 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Col 51-54; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                          89US-00312543.
89US-00441703.
91US-00715181.
92US-00872646.
                                                                                                                                                                                                                                                                                                                                                                                                                94US-00239276.
                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                    autoimmune disease; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24; Conservative
                               24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 24; Conserv
   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (FARB ) BAYER CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 294 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAV63560
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  DS-MAY-1994;
                                                                                                                                                                                                                  01-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                           17-FEB-1989;
04-DEC-1989;
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                                                                                                                                                                                                                                                                                                                                                          JS5840836-A.
                                                                                                                                                                                                                                                                                                                                                                                     24-NOV-1998
                                                                                                                                                                                     AAW80486;
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                              Matches
                                                                                                                              RESULT 3
AAW80486
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1 KLKVESSPSRSDYINASPIIEHDP 24

The present sequence represents a human pancreatic islet cell antigen (ICA) that binds with antibodies found in the sera of patients afflicted with insulin-dependent (Type 1) diabetes mellitus (IDDM). ICAS from the present invention are encoded by the DMA insert of a recombinant cloning vehicle selected from ATCC 40550 (AAZ22333, encoding AAM49847), ATCC 40553 (AAZ32334, encoding AAM49847), ATCC

New pancreatic islet cell antigens, useful in the diagnosis of insulin-

dependent (Type 1) diabetes mellitus.

Claim 1; Col 83-86; 61pp; English.

us-10-783-095-12.rai

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TYPE: PRT
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Sequence 19, Appl
Sequence 19, Appl
Sequence 19, Appl
Sequence 2, Appli
Sequence 41, Appli
Sequence 42, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 26, Appli
Sequence 27, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
                                                                October 28, 2004, 10:22:24 ; Search time 25.4458 Seconds (without alignments) 62.550 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 16,
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Sequence
Sequence
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                                                                                                                                                                                                                                                                                                                         Issued Patents AA:*

(cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-468-5778-18

US-08-468-5778-18

US-08-468-578-19

US-08-468-578-19

US-08-468-5778-19

US-08-468-5778-19

US-08-015-339-54

US-09-552-8028-42

US-09-876-527-4

US-08-811-481-2

US-08-811-481-2

US-08-811-481-2

US-08-811-481-2

US-08-811-481-2

US-08-811-481-2

US-08-811-481-2

US-08-811-481-2

US-08-811-481-2

US-08-811-481-16

US-08-811-481-16
                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JS-08-884-569A-2
                                                                                                                                                                                              478139 segs, 66318000 residues
                                                                                                                                       24
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                                                                                                                                                                                                                                                                            Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries
                                            OM protein - protein search, using sw model
                                                                                                             US-10-783-095-12
123
1 KLKVESSPSRSDYINASPIIEHDP
                                                                                                                                                            BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match
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Perfect score:
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                                                                                                                                                                                               Searched:
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No.
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Sequence 38, Appl
Sequence 52, Appl
Sequence 46239, A
Sequence 5529, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 14989, A
Sequence 809, Appli
Sequence 809, Appli
Sequence 214989, A
Sequence 25959, A
Sequence 25959, A
Sequence 25959, A
Sequence 23, Appli
US-09-552-802B-38
US-09-552-802B-39
US-09-552-802B-52
US-09-270-767-46239
US-09-355-214-3
US-08-819-013-1
US-09-355-214-1
US-09-358-214-1
US-09-358-214-1
US-09-358-214-1
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US-09-358-214-1
US-09-358-092-809
US-09-358-092-809
US-09-793-998-8
US-09-793-998-8
US-09-793-998-8
US-09-134-61A-6130
US-09-252-991A-25959
US-09-444-955-23
US-09-252-91A-17298
US-09-252-91A-17298
US-09-252-91A-17298
```

```
## Second Control of Application US/08884569A

## Special Control of Application US/08884569A

## Patent No. 6399326

## Patent No. 6399326

## Patent INFORMATION:

## APPLICANT: CHIANGAM, MING-KO

## APPLICANT: TEANAGAM, JOHN G.

## TITLE OF INVENTION: RECEPTOR TYROSINE PHOSPHATASE, AND USES RELATED THERETO

## FILE REFERENCE: HWW-020.01

## CURRENT APPLICATION NUMBER: 06/021,040

## PRIOR PILING DATE: 1996-07-02

## NUMBER OF SEQ ID NOS: 15

## SOFTWARE: PatentIn Ver. 2.1

## SEQ ID NO 4

## INFORMET STATES

## INFORMET SEQ ID NO 4

## INFORMET SEQ ID NO 4

## INFORMET SEQ ID NO 4

## INFORMET SEQ ID NO 4
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US-08-468-576B-18

Sequence 19, Application US/08468576B

Patent No. 595345

GENERAL INFORMATION:

APPLICANT: Rabin, Daniel

TITLE OF INVENTION:

NUMBER OF SEQUENCES: 19

CORRESPONDED: ADDRESS:

ADDRESSEE: Sprung Kramer Schaefer & Briscoe

STREET: 660 White Plains Road

CITY: Tarrytown

STATE: New York

COMPUTRY: USA

COMPUTRY: USA

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage

COMPUTER: Apple Macintosh

COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 123; DB 3;
100.0%; Pred. No. 1.1e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19 KLKVESSPSRSDYINASPIIEHDP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 KLKVESSPSRSDYINASPIIEHDP 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ) ORGANISM: Mus sp. US-08-884-569A-4
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Length 294;
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ZIP: 10:59 U-54

ZIP: 10:59 U-54

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintcohn
OPERATING SYSTEM: System 7.5

SOFTWARE: Wordferfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,577B
FILING DATE: 06-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 04-DEC-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 18, Application US/08468577B
; Sequence 18, Application US/08468577B
; Patent No. 6001804
; GENERAL INFORMATION:
APPLICANT: Rabin, Daniel
; TITLE OF INVENTION: PANCEBATIC ISLET CELL ANTIGENS
; TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sprung Kramer Schaefer & Briscoe
; STREET: 660 White Plains Road
; CITY: Tarrycown
; STREE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
100.0%; Score 123; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.4e-12;
Matches 24; Conservative 0; Mismatches 0;
     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-7UN-1991
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/441,703
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/312,543
FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: KULF G. BELSEGOR
REGISTRATION NUMBER: 33.141
REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (914) 332-1700
TELEFAX: (914) 332-1844
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 294 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
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US-08-468-577B-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 18, Application US/08468579B
Sequence 18, Application US/08468579B
Sequence 18, Application US/08468579B
SEQUENCE INFORMATION:
TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS
TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
NUMBER OF SEQUENCES: 19
CORRESONDENCE ADDRESS:
ADDRESSEE: Sprung Kramer Schaefer & Briscoe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 10591-5144
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
COMPUTER: Apple Macintosh
OPERATING SYSTEM: System 7.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Sprung Kramer Schaefer & Briscoe STREET: 660 White Plains Road CITY: Tarrytown STATE: New York
                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-UNN-1992
FILING DATE: 08-UNN-1991
FILING DATE: 14-UNN-1991
FILING DATE: 14-UNN-1991
FILING DATE: 14-UNN-1991
FILING DATE: 14-UNN-1991
FILING DATE: 04-DEC-1989
FILING DATE: 04-DEC-1989
FILING DATE: 17-FEB-1989
FILING DATE: 17-FEB-1989
ATTORNEY/ABOUT INFORMATION:
NAME: KURT G. BTISCOG
REGISTRATION NUMBER: 33,141
REFERENCE/DOCKET NUMBER: 33,141
REFERENCE/DOCKET NUMBER: 33,141
FELECOMMUNICATION INFORMATION:
TELEPHONE: (914) 332-1700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-190A
                       CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,576B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
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FILING DATE: 05-YAY-1994
PROOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 294 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Conservative
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CURRENT APPLICATION DATA
APPLICATION NUMBER: US
WordPerfect
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Best Local Similarity
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US-08-468-579B-18
SOFTWARE:
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Gaps

· 0 Sequence 196840, Sequence 8, Appli Sequence 6573, Appli Sequence 221903, Sequence 111307, Sequence 11307, Sequence 15261, Appli Sequence 2455, Appli Sequence 2455, Appli Sequence 62602, A Sequence 62602, A Sequence 6763, A Sequence 12, Appli Sequence 1824, Appli Sequence 182

Sequence 7255, Ap Sequence 9, Appli Sequence 2511, Ap Sequence 196840,

Sequence 38, Appl Sequence 39, Appl Sequence 52, Appl Sequence 115384, Sequence 189618,

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S US-10-378-479-40

S US-10-378-479-38

S US-10-378-479-38

S US-10-378-479-52

6 US-10-437-963-115384

4 US-10-032-585-7255

4 US-10-032-585-7255

4 US-10-032-585-7255

4 US-10-177-478-9

US-10-437-963-11937

6 US-10-437-963-11307

6 US-10-447-99-136-80

6 US-10-447-99-131675

6 US-10-447-99-131675

6 US-10-447-99-131675

6 US-10-447-963-11807

6 US-10-447-963-11807

6 US-10-447-963-11807

6 US-10-447-963-11807

6 US-10-459-144-66408

5 US-10-425-114-66408

5 US-10-425-114-66408

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6 US-10-425-114-66408

6 US-10-425-114-69763

6 US-10-425-200-1824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-038-686-3
Sequence 3, Application US/10038686
Publication No. US2030044467A1
SEGNERAL INPORMATION:
APPLICANT: Orban, Tihamer
FILE REFERENCE: 10276-067701
CURRENT APPLICATION NUMBER: US/10/038,686
CURRENT APPLICATION NUMBER: 05/060,068
PRIOR PLING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FasteED for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KLKVESSPSRSDYINASPIIEHDP 775
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Sequence 41, Application US/10378479
Publication No. US20040006202A1
GENERAL INFORMATION:
APPLICANT: Peakman, Mark
APPLICANT: Chicz, Roman M.
       , ORGANISM: Homo sapiens
US-10-038-686-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 979
TYPE: PRT
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65.55
74.55
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Sequence 42, Appl
Sequence 42, Appli
Sequence 4, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 2, Appli
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Sequence 22, Appl
Sequence 22, Appl
Sequence 16, Appl
Sequence 16, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                             October 28, 2004, 10:54:39 ; Search time 313.735 Seconds (without alignments) 24.802 Million cell updates/sec
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(gnz 16/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
(gnz 16/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
(gnz 16/ptodata/2/pubpaa/USO6 PUBCOMB.pep:*
(gnz 16/ptodata/2/pubpaa/USO7 NW PUB.pep:*
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(gnz 16/ptodata/2/pubpaa/USO9 PUBCOMB.pep:*
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(gnz 16/ptodata/2/pubpaa/USO0-PUBCOMB.pep:*
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                             GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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5 US-10-378-479-41

US-10-378-479-42

US-10-378-479-42

US-10-18-689-4

US-10-124-089-4

US-10-124-089-2

US-10-124-089-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hits satisfying chosen parameters:
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123
1 KLKVESSPSRSDYINASPIIEHDP 24
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Applications AA:*
                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                 1370721 seqs, 324215800
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0 seq length: 2000000000
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Match Length DB
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                             Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB
Maximum DB
                                                                                                                                                                                                                                                                                                                Sequence:
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No.
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ALIGNMENTS

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Gaps

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Length 979; Indels

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TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                   NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS
                                                                                                                                            Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Seattle
                                                                                                                                                                                              COUNTRY: USA
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US-10-378-479-42

US-10-378-479-42

Sequence 42, Application US/10378479

Publication No. US2004006202A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Chicz, Roman M.
TITLE OF INVENTION: REPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
TITLE OF INVENTION: DEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
TITLE OF INVENTION: DEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
TITLE OF INVENTION: DEPTIDE 2003-03-03
CURRENT FILING DATE: 2003-03-03

PRIOR PRIOR PRILOR DATE: 2003-04-20

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

PRIOR FILING DATE: 1999-04-21

NUMBER OF SEQ ID NOS: 55

SECTIVARE FESTSEQ FOR Windows Version 4.0
TITLE OF INVENTION: PEPTIDE EPITOPES RECOGNIZED BY DISEASE PROMOTING
TITLE OF INVENTION: CD4+T LYMPHOCYTES
FILE REPRENCE: 08191-009002
CURRENT APPLICATION NUMBER: US/10/378,479
CURRENT APPLICATION NUMBER: US/10/378,479
CURRENT FILING DATE: 2003-03-03
PRIOR PEPLICATION NUMBER: US/09/52,802B
PRIOR PELLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 09/295,868
PRIOR APPLICATION NUMBER: US 60/130,355
PRIOR APPLICATION NUMBER: US 60/130,355
PRIOR FILING DATE: 1999-04-21
NUMBER OF SEQ ID NOS: 55
SOFTWARE: FastSEQ for Windows Version 4.0
LENGTH: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 74.8%; Score 92; DB 15; Length 19; Best Local Similarity 100.0%; Pred. No. 4.1e-07; Matches 19; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 KVESSPSRSDYINASPIIEHDP 24
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LaGasse, James M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/09876527
Patent No. US20020102616A1
GENERAL INFORMATION:
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Jelinek, Laura J.
Sheppard, Paul O.
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                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: Homo sapiens
US-10-378-479-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-10-378-479-41
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                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastESE for Windows Version 2.0
CURBNY APPLICATION DATA:
APPLICATION NUMBER: US/09/876,527
FILING DATE: 07-Jun-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION NUMBER: 08/911,481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 74.0%; Score 91; DB 9; Le Best Local Similarity 73.9%; Pred. No. 1.4e-05; Matches 17; Conservative 3; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LAĞASSE, James M.
TITLE OF INVENTION: ISLET CELL ANTIGEN 1851
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: ZymcGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: ZymoGenetics, Inc.
STREET: 1201 Eastlake Avenue East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
HOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-876-527-4
                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Lingenfelter, Susan
REGISTRATION NUMBER: P-41,156
REFERENCE/DOCKET NUMBER: 95-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              150 LKAENSHSHSDYINASPIMDHDP 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 LKVESSPSRSDYINASPIIEHDP 24
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Sheppard, Paul O.
Hagopian, William A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6675
TELEFAX: 206-442-6678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
US-10-124-089-4
US-10-124-089-4
; Sequence 4, Application US/10124089;
; Publication No. US20030166067A1
; GENERAL INFORMATION:
APPLICANT: Animak. Laura J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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979
100.0
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                                                                                                                      October 28, 2004, 10:55:55; Search time 77.5904 Seconds (without alignments) 129.454 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                 Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                   US-10-783-095-11
28
1 LAKEWQALCAYQAEPNTCATAQGEGNIK 28
                                                                                                                                                                                                                                                                                                                                        2002273 seqs, 358729299 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                     - protein search, using sw model
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Gapop 60.0 , Gapext 60.0
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geneseqp2003as:*
geneseqp2003bs:*
geneseqp2004s:*
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                                   OM protein
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Result No.	Score	Query Match	Query Match Length	DB	ID	Description
	i (N	100.0	. 2	. 0	AAY33360	Aav33360 Human isl
73	28	100.0	~	N	AAY49854	4 Human
т	73	100.0	294	~	AAW80486	6 Islet
. 4	28	100.0	N	m	AAY49329	29 Pancre
5	28	100.0	m	m	AAY59351	_
9	28	100.0	ស	7	AAY33361	Н
7	28	100.0	ഹ	~	AAY49855	Human
80	28	100.0	Ŋ	~	AAW80487	3487 Islet
6	28	100.0	ľ	m	AAY49330	
10	28	100.0	Ŋ	9	ABU04788	
11	78	100.0	w	9	O)	
12	28	100.0	Ŋ	9	ABU04792	Human
13	28	100.0	ιO	9	ABU04791	Human
14	28	100.0	w	9	ABU04783	Abu04783 Human exp
13	28	100.0	M	9	ABU04785	5 Human
16	28	100.0	w	9	ABU04795	Human
17	28	100.0	σ	7	ADE56165	Rat Pr
80	78	100.0	σ	7	ADD45276	Rat
13	28	100.0	σ	ഹ	Н	സ്
20	28	100.0	σ	7	AAY06606	Aay06606 Human isl
21	28	100.0	979	4	AAG80205	Human
22	28	100.0	979	Ø	ABU04793	Abu04793 Human exp
23	79	100.0	979	φ	ABU04784	Abu04784 Human exp
24	28	100.0	979	9	ABU04789	Abu04789 Human exp
25	28	100.0	979	9	ABU04794	4 Human

Ade57230 Human ProAde57226 Human ProAd45722 Human ProAd45722 Human ProAd45722 Human ProAd657222 Human ProAd65722 Human ProAd65722 Human ProAd5729 Prpase PrAD40478 Human expAD404787 Human expAD4787 Human expAD60054 CRH signa AD657041 Mouse iscAD30255 CD4+ T-ceAD30255 CD4+ T-ceAD	NTS				protein fragment.	as; antibody; IDDM; immunoassay; itus; diagnosis; immunoglobulin; ; immunoreactivity; disease; creening.						DIAGNOSTIC.			e with serum from diabetics useful and monitoring of insulin-dependent		ated and purified DNAs encoding trive with islet cell antibodies found spendent type I diabetes mellitus fention are useful as immunoassay grosis of insulin-dependent type I ity of the polypeptides to bind the
ADE57230 ADE56167 ADE57286 ADE57218 ADE57218 AAB30260 AAB30260 AAB459337 AAB30259 AAB30259 AAB30259 AAB30255 AAB30255	ALIGNMENT	294 AA.			one ICA-512	an; pancrea betes melli estruction; antigen; sc						MOLECULAR			s reactive iagnosis a	lish.	isol reac in-de in-de
		i,		Ś	clor	hum dia 1 d				576.	181. 181. 646.	RLY M			igen he d	Engl	novel tigens insul: of the
000000 00000 000000 000000 0000000000		; protei		st entry	antigen	n; ICA; type I slet cel				5US-00468	US-00312 US-00441 US-00715 US-00872 US-00239	P FORMER			ling ant s for t	, 63pp;	invention describes interactic fisher cell antisers of partients with MN. The polypeptides ents in the presymptometes mellitus (IDDM).
00000000000000000000000000000000000000		andard		(fir	11	ige int				196	891 891 911 921	CORE		94/4 22.	ncod duct tus.	5-87	des et c ient lype e pr
000000000000000000000000000000000000000		th ch		0	t Ge	ant: pend( cell rapy	ns.	Ä.		5;	00104	YER		5604 2099	DNA e p pro melli	Col 8	tion fal pat Pot Po
2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2		. 1 60 AY33360 s	Y33360;	-NOV-199	Human isle	let cell sulin-de sell; B-	mo sapien	5955345-	-SEP-199	- JUN-199	-FEB-198 -DEC-198 -JUN-199: -JUN-199:	ARB ) BAY	abin DU;	I; 1999-9 PSDB; AA	olated Di develop abetes me	Example; Co	
ИИИИММММММММ 4 4 4 4 4 ФГВООТИМ4 5 ФГВООТИМ4 11		3336 3336 AA	AAY		Hul	ins ins in-c	Ношо					(FAR	Ral		Iso to dia	EX	Thi pan in (ID rea dia
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antibody binding site on islet cell antibodies (ICAs) also confers
utility in the binding or blocking of human immunoglobulin, T-cells, or B
cells involved in IDDM. The products can also be used to study the
biological mechanisms involved in islet cell destruction and the
appearance of ICA. The immunoreactivity profile with different antigens
an provide diagnostically significant information concerning the native
of the disease, e.g. subtypes, the state of the disease, the proximity to
onset of the disease, and the efficacy of therapy, e.g. immune therapy.
The antigens can serve as stimulating antigens for T-cell culture, permitting significantly improved T-cell cloning, identification, and
growth. The availability of large quantities of pure antigen enables the
development of highly sensitive and specific immunoassays which can be
used to screen the general population of presymptomatic IDDM or a
providence of the purpose of the property of the providence represents the human islet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents a human pancreatic islet cell antigen (ICA) that binds with antibodies found in the sera of patients afflicted with insulin-dependent (Type 1) diabetes mellitus (IDDM). ICAs from the present invention are encoded by the DNA insert of a recombinant cloning vehicle selected from ATCC 40550 (AAZ32333, encoding AAX49847), ATCC 40553 (AAZ32334, encoding AAX49848), ATCC 40554 (AAZ32335, encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New pancreatic islet cell antigens, useful in the diagnosis of insulindependent (Type 1) diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human pancreatic islet cell antigen ICA-512 ATCC 40706 protein.
                                                                                                                                                                                                                                                                                                                                  100.0%; Score 28; DB 2; Length 294; 100.0%; Pred. No. 1.2e-21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, pancreatic islet cell antigen, ICA clone, IDDM, insulin dependent type I diabetes mellitus, diagnosis; immunoglobulin, T-cell, B-cell, antibody binding.
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                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                  67 LAKEWQALCAYQAEPNTCATAQGEGNIK 94
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                                                                                                                                                                                                                                                              cell antigen from clone ICA-512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY49854 standard; protein; 294
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89US-00441703.
91US-00715181.
92US-00872646.
94US-00239276.
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                                                                                                                                                                                                                                                                                                     Sequence 294 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            04-DEC-1989;
14-JUN-1991;
08-JUN-1992;
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(AAZ32337, ALUC 4U551 (AAZ32336, encoding AAY49850), ATCC 40552
ATCC 40704 (AAZ32337, encoding AAY49851), ATCC 40703 (AAZ32338, encoding AAY49852),
ATCC 40706 (AAZ323319, encoding AAY49853), ATCC 75030 (AAZ32340), ATCC
AAX49855). ICA proteins and their peptide fragments can be used in the diagnosis of IDDM and in detecting or blocking human immunoglobulin, T-cells or B-cells involved in IDDM
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                                                                                                                                                                                           Gaps
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treatment; insulin dependent diabetes mellitus; IDDM; autoantibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptide antigens from pancreatic islet cells - useful for the detection and treatment of insulin dependent diabetes mellitus.
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                                                                                                                                                             100.0%; Score 28; DB 2; Length 294; 100.0%; Pred. No. 1.2e-21; ive 0; Mismatches 0; Indels
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ilarity 100.0%; Pred. No. 1.2e-21;
Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                67 LAKEWQALCAYQAEPNTCATAQGEGNIK 94
                                                                                                                                                                                                                                                                                                                                AAW80486 standard; protein; 294 AA
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89US-00441703.
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92US-00872646.
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Best Local Similarity
Matches 28; Conserv
                                                                                                                                                                               Best Local Similarity
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14-JUN-1991;
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ID AAW8
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